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FILING DATE: 2000-11-08
APPLICATION NUMBER: PCT/USO0/30873
FILING DATE: 2000-11-10
FILING DATE: 2000-11-10
APPLICATION NUMBER: PCT/USO0/32678
APPLICATION NUMBER: US 09/747, 259 FILING DATE: 2000-07-25 APPLICATION NUMBER: PCT/US00/20710 FILING DATE: 2000-10-24
APPLICATION NUMBER: US 09/709, 238
FILING DATE: 2000-11-08
APPLICATION NUMBER: PCT/US00/30952 FILING DATE: 2000-12-20 APPLICATION NUMBER: PCT/US00/34956 FILING DATE: 2001-02-28 APPLICATION NUMBER: PCT/US01/06520 APPLICATION NUMBER: PCT/US01/06666 FILING DATE: 2001-03-01 APPLICATION NUMBER: US 09/802,706 APPLICATION NUMBER: PCT/US01/17800 FILING DATE: 2001-06-01 FILING DATE: 2001-06-20
APPLICATION NUMBER: PCT/US01/00000 APPLICATION NUMBER: PCT/US01/17092 FILING DATE: 2001-05-25 APPLICATION NUMBER: PCT/US01/17443 LICATION NUMBER: PCT/US00/23522 APPLICATION NUMBER: PCT/US00/23328 APPLICATION NUMBER: PCT/US01/19692 APPLICATION DATE: 2000-07-20 APPLICATION NUMBER: US 60/220,624 TITING DATE: 2000-07-25 TITING DATE: 2000-07-25 APPLICATION NUMBER: US 60/222,695 FILING DATE: 2000-08-02 APPLICATION NUMBER: US 60/230,978 us 60/000,000 FILING DATE: 2000-09-15 APPLICATION NUMBER: US 09/664,610 FILING DATE: 2000-09-18 FILING DATE: 2000-09-18 APPLICATION NUMBER: US 60/242,922 FILING DATE: 2000-12-20 PPLICATION NUMBER: US 09/767,609 FILING DATE: 2001-01-22 APPLICATION NUMBER: US 09/796,498 FILING DATE: 2001-03-09 APPLICATION NUMBER: US 09/808,689 APPLICATION NUMBER: US 09/816,744 FILING DATE: 2001-03-22 APPLICATION NUMBER: US 09/828,366 APPLICATION NUMBER: US 09/854,280 FILING DATE: 2001-05-10 FILING DATE: 2001-05-25 APPLICATION NUMBER: US 09/866,034 APPLICATION NUMBER: US 09/870,574 APPLICATION NUMBER: US 09/643,657 APPLICATION NUMBER: US 09/665,350 APPLICATION NUMBER: US 09/854,208 APPLICATION NUMBER: US 09/866,028 APPLICATION NUMBER: US 60/219,556 2001-03-14 2001-05-10 2000-09-07 2000-07-28 2000-08-17 2000-08-24 2001-02-28 2001-04-05 2001-05-25 2001-05-30 2000-08-23 FILING DATE: 2001-05-30 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: FILING DATE: LING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR

283 ctggccaagcagaaggcccaggaagctgagaaattgctgaacaatgtcatttctaagctg 342 343 cttccaactaacacggacatttttgggttgaaaatcagcaactccctcatcctggatgtc 402 583 gaatgegeeautgacceaaccageateteacttecttgetggacaaacagecaaatc 642 43 totgaggtggtgtcaagacaaaagatgettcagetttggaaacttgtteteetgtgegge 102 85 GTGCTCACTGGGACCTCAGAGTCTCTTGTTGACAATCTTGGCAATGACCTAAGCAATGTC 144 145 GIGGATAAGCIGGAACCIGITCITCACGAGGGACTIGAGACAGTIGACAATACICITAAA 204 163 giggataagciggaaccigitetteacgagggactigagacagtigacaatactettaaa 222 205 GCCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAA 264 223 ggcatcottgagaaactgaaggtcgacctaggagtgcttcagaaatccagtycttggcaa 282 265 CTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAATTGCTGAACAATGTCATTTCTAAGCTG 324 325 CTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTC 384 385 AAAGCTGAACCGATCGATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAAT 444 445 GTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTC 504 505 CTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGA 564 523 ctgaccgcagtcacaattgaaactgatccccagacaccaccagcctgttgccgtcctggga 582 565 GAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGGTGGACAAACACAGCCAAATC 624 625 ATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTG 684 643 atcaacaagttegtgaatagegtgateaacaegetgaaaaageactytateeteeetgetg 702 685 CAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATT 744 745 CAGCAGGICGICGAIAAICCICAGCACAAAACCCAGCIGCAAACCCTCAITIGAAGAGGA 804 763 cagcaggiogicgiataaicotcagcacaaaacocagoigcaaacoctcatoigaagaga 822 823 cgaatgaggaggaccactgtggtgcatgctgattggttcccagtggcttgccccacccc 882 805 CGAATGAGGAGCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCC 864 865 TTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCTAACCAGCGTGAAAGCCTGAGTC 924 0; Gaps 25 TCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGC 84 96.3%; Score 990.4; DB 37; Length 1049; 99.4%; Pred. No. 5.8e-269; 6; Indels 0; Mismatches PRIOR FILING DATE: 2001-06-28 NUMBER OF SEQ ID NOS: 383 SEQ ID NO 163 Query Match
Best Local Similarity 99.4%
Matches 994; Conservative TYPE: DNA ORGANISM: Homosapiens US-10-081-056-163 1049 LENGTH: ó δλ a ò g g q ò g g ò à ò g ô DP ô a g ò qq ò βp ò

us-10-020-139-1.rnpm

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TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 824 base pairs
TYPE: nucleic acid
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TILLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYMUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
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                   43 tetgaaggtggtgteaagacaaaagatgetteagetttggaaaettgtteteetgtgegge 102
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                                                                      985 CATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCA 1024
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OTHER INFORMATION: Incyte ID No: 903509.6
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CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                  Sequence 33384, Application US/60324185 GENERAL INFORMATION:
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                                                                                                                                                                                  US-60-324-185-33384
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583 gaatgegeeagtgaceeaaceageateteaettteettgetggacaaacacageeaate 642
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                                                                                                                     625 ATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTG 684
                                                                                                                                                                                     643 atcaacaagttcgtgaatagcgtgatcaacacgctgaaaagcactgtatcctcctgctg 702
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565 GAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGGTGGACAAACACAGCCAAATC 624
                                                                                                                                                       Incyte Pharmaceuticals, Inc.
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PAROTID
TITLE OF INVENTION: SECRETORY PROTEIN
NUMBER OF SEQUENCES: 5
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FastSEQ Version 2.0
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                                                                                                                                                                                                                           5 GATTICATGAGCATCCTCTAAACGCGTGTCAAAGACAAAAGATGCTTCAGCTTTGGAA 64
                                                                                                                                                             0;
                                                                                                                 Score 818.4; DB 11; Length 824; Pred. No. 2.5e-220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOVEL NUCLEIC ACID MOLECULES AND USES
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// GENERAL INFORMATION:
                                                                                                                      79.68;
99.98;
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TITLE OF INVENTION: NOVEL NO
                                                                                                                                                               Conservative
TOPOLOGY: linear
                                         CLONE: Consensus
                                                                                                                      Query Match
Best Local Similarity
Matches 819; Conserv
                 IMMEDIATE SOURCE:
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Sequence 2204, Application US/60250830
GENERAL INFORMATION:
APPLICANT: MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
APPLICANT: Diep, Dinh
APPLICANT: Diep, Dinh
APPLICANT: Diep, Dinh
AFTHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USIN
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
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                                                                                                                                                                           FastSEQ for Windows Version 4.0
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                     FILE REFERENCE: 1600.1194-001
CURRENT APPLICATION NUMBER: US/09/652,122
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,421
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 5020
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pr
tive 0;
  THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 631; Conservative
                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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Best Local Similarity
TITLE OF INVENTION:
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                                                                                                                                                                                                SEQ ID NO 2764
                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                           SOFTWARE:
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Search completed: August 6, 2002, 18:16:39
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           LENGTH: 501
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FILE REPERENCE: GX-0020-1 P
CURRENT APPLICATION NUMBER: US/60/323,966
CURRENT FILING DATE: 2001-09-21
NUMBER: OF SEQ ID NOS: 3246
SOFTWARE: PERL PROGRAM
SEQ ID NO 2204
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TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY FILE REFERENCE: GX-0020 P CURRENT APPLICATION UNMBER: US/60/250,830 CURRENT FILING DATE: 2000-11-04 NUMBER OF SEQ ID NOS: 3246 SOFTWARE: PERL Projram SEQ ID NO 2.204
                                                                                                                                                                                                                                                                                                                                       Query Match 48.6%; Score 499.4; DB 64.
Best Local Similarity 99.8%; Pred. No. 3.8e-130;
                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
O OTHER INFORMATION: Incyte ID No: 903509.9
15-66-250-830-2204
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APPLICANT: Diep, Dinh
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                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                         0; Mismatches
                                                                        NAME/KRY: misc_feature
CTHER INFORMATION: Incyte 1D No: 903509.9
US-60-323-966-2204
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                                                                                                                                                                                                                                                                         Matches 500; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
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Wed Aug, 7 05:46:10 2002

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; Search time 219.26 Seconds (without alignments) 10202.412 Million cell updates/sec
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9, Appli
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Sequence 11687, A
Sequence 18, Appl
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1 Cacuadatticatgaggaic......aagggcgattigfgcaaaaa 1028
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Sequence 434,
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1: /cgn2_6/ptodata/1/pna/VCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*
                  Copyright (c) 1993 - 2000 Compugen Ltd.
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US-10-020-139-11
US-10-020-139-11
US-10-020-139-14
US-10-020-139-14
US-10-020-139-15
US-10-020-139-16
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US-10-020-139-16
US-10-020-139-16
US-10-020-139-18
US-10-020-139-18
US-10-020-139-18
US-10-176-912-434
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US-10-192-254-9
US-10-184-638-373
US-10-187-594-373
US-10-187-743-373
US-10-187-748-373
                                                                                                                                                                                              1362792 segs, 1088025756 residues
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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US-10-187-589-373
         GenCore version 4.5
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                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
                                                                        August. 6, 2002, 16:52:46
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 373,
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COMPUTER: IBM PC Compatible
SPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Parotid Secretory Protein
US-10-187-590-373
US-10-187-591-373
US-10-187-600-373
US-10-187-746-373
US-10-187-746-373
US-10-187-751-373
US-10-187-753-373
US-10-187-753-373
US-10-187-753-373
US-10-187-753-373
US-10-187-754-373
US-10-187-885-373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT TREPRATION NUMBER: US/08/993,529
FILING DATE: <URNOWN>
ATTORNEY/AGENT TREPRATION:
NEGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF348
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APPLICATION NUMBER: US/10/020,139
FILING DATE: 18-Dec-2001
CLASSIFICATION: «Unknown>
PKIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 301-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1028 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10020139
GENERAL INFORMATION:
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49..100
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                      121 CTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTT 180
                                                                                                                                                                                                                                                                          GAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTG 240
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                                                                                 100.0%; Score 1028; DB 7; Length 1028; 100.0%; Pred. No. 9.8e-281;
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                        ; SEQUENCE DESCRIPTION: SEQ 1D NO: 1: US-10-020-139-1
                                                                                                              Conservative
NAME/KEY:
                                                                                                Similarity
             LOCATION:
                                                                                                              Matches 1028;
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                     961 ACAGTCAGAACAGCAGCCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTC 1020
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 GTGCTCACTGGGACCTCAGAGTCTCTTTGACAATCTTGGCAATGACCTAAGCAATGTC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 gigotoactgggacotcagagtototlottgacaatottggcaatgacotaagcaatgto 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 GGCATCCTTGAGAAACTGAAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 CTGGCCAAGCAGAAGGCCCAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 AAAGCTGAACCGATCGATGATGCCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAAT 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 990.4; DB 7; 99.4%; Pred. No. 4.3e-270;
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Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: P3530PICI
CURRENT PPLICATION NUMBER: US/10/119,480
CURRENT FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 246
                                                                                                                                                                                                                                                                                                                                                                                                      Stephan, Jean-Philippe F. Watanabe, Colin L. Wood, William I.
                                                                                                                                                                                                                       ; Sequence 159, Application US/10119480
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.48
Matches 994; Conservative
                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapien
                                                                             1021 TGCAAAA 1028
                                                                                                                  1021 TGCAAAAA 1028
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APPLICANT:
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                                           523 ctgaccgcagtcacaattgaaactgatccccagacaccccagcctgttgccgtcctggga 582
                                                                                                                              583 gaatgegeeagt.gacceaaceageateteaettteettgetggacaaacacageeaaate 642
                                                                                                                                                                                                                      643 atcaacaaylloyigaatagogigatoaacaacgotgaaaaagcacigtatootoootgotg 702
                                                                                                                                                                                                                                                                                                       703 cagaaggagalatgtccactgatccgcatcttcatccactccctggatgtgaatgtcatt 762
                                                                                                                                                                                                                                                                                                                                                                       883 ttatagcatctccctccaggaagctgctyccaccacctaaccagcgtyaaagcctgagtc 942
565 GAATGCGCCAGTGACCCGAACCAGCATCTCACTTTCCTTGCTGGACAACACAGGCCAAATC 624
                                                                                                                                                                          625 ATCAACAAGTIFGTGAATAGCGTGATCAACAGGTGAAAAGCACTGTATCCTGCTGCTG 684
                                                                                                                                                                                                                                                             685 CAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACCCCTGGATGTGAATGTCATT 744
                                                                                                                                                                                                                                                                                                                                                745 CAGCAGGICGICGAIAAICCICAGCACAAAACCCAGCIGCAAACCCTCAITIGAAGAGGA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                   805 CGAATGAGGAGCACTGTGGGGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            925 CCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTACA 984
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STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/020,139
FILING DATE: 18-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEFAX: (301) 301-8439
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RUBEN, STEVEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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183 GAGACAGTTGACAATACTCTTAAAGGGCATCCCCNTTTNGAGAAACTGAAGGTCGACCT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TGGAAACTTGTTCTCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTCTTGACAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 TGGAAACTTGTTCTCCTGTGCGGCGTGCTCACGGGACCTCCAGAGTCTCTTGACAAT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 AGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGA 293
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                      1 CACGAGATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GAGACAGTTGACAATACTGTTAAAGG-----CATCCTTGAGAAACTGAAGGTCGACCT
                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                             DB 7; Length 449;
                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Parotid Secretory Protein NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                    . 6e-98;
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STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                          37.3%; Score 383.8;
95.5%; Pred. No. 1.6e
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/020,139
                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-020-139-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 GGCCTTAACCTGAGCTTCCCTGTCACC 438.
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10020139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                         LENGTH: 449 base pairs
                                                TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DUAN, ROXANNE
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                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                 Local Similarity
nes 427; Conserv
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CITY: ROCKVILLE
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGTTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 TCATCCTGGATGTCAAAGCTGAACCGATCGATGGTGGAAAGGCCTTAACC----TGAGC 426
                                                                                                                                                                                                                                                                                                                                                                                       54; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               12 ATGAGCATCCTCCTCTAAACGCGGTGTCAAGACAAAAGATGCT-TCAGCTTTGGAAACTTG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAGCATCCTCCTCTAAACGCGGTGTCAAGACAAAAGATGCTNNCAGCTTTGGAAACTTG 60
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STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                               REFERENCE/DOCKET NUMBER: PF348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ 1D NO: 11:
SEQUENCE CHARACTERISTICS:
             ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
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GENERAL INFORMATION:
APPLICANT: DUAN, ROXANNE
                                                                                                                                                                                 LENGTH: 538 base pairs
<Unknown>
                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 87.79
Matches 469; Conservative
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                                                                                                                                                                                                                                                                                                 US-10-020-139-11
                                                                                                                                                                                                                                                                                                                                                         Query Match
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63 TGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTCTTGACAAT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTCTTCTTGACAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CTTGGCAATGACCTAAGCAATGTCGTGGATAAGCT-GGAACCTGTTCTTCACGAGGGACT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 GCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGGAAGG-CCCAGGAAGCTGAGAAAT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CACGAGATTTCATGAGCATCCTCCTCTAAACGCGTGTCAAAGACAAAAGATGCTTCAGCTT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CACGAGATTTCATGAGCATCCTCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTT 60
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Parotid Secretory Protein
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                          APPLICATION NUMBER: US/10/020,139
FILING DATE: 18-Dec-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: DAR (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-020-139-12
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                          NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/10020139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 301-8439
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 359 base pairs
                                                                                                                                                                                                                                                                                                              <Unknown>
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 347; Conservative
                                                                                                                                                                                                                                                                                                              FILING DATE:
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Best Local Similarity
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NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 301-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 406 base pairs
                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 89.4%;
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 313; Conservative
                                                                                                          SO
                                                                                                                     ZIP: 20850
                                                                                       STATE: MD
                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-020-139-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     824 TGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCAGCCCCTTATAGCATCTCCCCAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          884 GAAGCIGCTGCCACCACCTAACCAGCGTGAAGCCT-GAGTCCCACCAGAAGGACCTTCC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              943 CAGATACCCC-TTCTCCTCACAGTCAGAACAGCAG--CCTCTACACATGTTGTCCTGCCC 999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/020,139
FILIAN DATE: 18-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Parotid Secretory Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%; Score 303.6; DB 7
95.0%; Pred. No. 7.5e-76;
tive 0; Mismatches 14
                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/993,529 FILING DATE: <Unknown>
                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF348
                                                                                                                                                                                                                                                                          NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 301-8439
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-10-020-139-14
Sequence 14, Application US/10020139
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 374 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DUAN, ROXANNE
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                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                              20850
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60 TGTTCTCTGTGCGGCGTGCTCACTGGGACTCTCTTCTTGACAATCTTGGCAA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 TGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCACGAGGGACTTGAGACAGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 TGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGTCGACCTAGGAGTGCTTCAGAA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 ITCATGAGCATCCTCCTCTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTTTGGAAACT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 -- AACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUAAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/020,139
FILING DATE: 18-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/10020139
GENERAL INFORMATION:
APPLICANT: DUAN, ROXANNE
RUBEN, STEVEN
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us-10-020-139-1.rnpn

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ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 17, Application US/10020139
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 395 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
                                                    CITY: ROCKVILLE
                                                                                                 ns
                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1025 AAAA 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 TGCTGGACAAACACCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  782 TGCAAACCCTCATTTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 TGTTTTCCAGACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 AAAGCACTGTTTCCTTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     722 ACTCCCTGGATGTGAATGTCATTCAGGAGGTCGTCGATAATCCTCAGCACAAAACCCAGC 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 ACTCCCTGGATGTGAATGTCATTCAGGAGGTCGTCGATAATCCTCAGCACAAAACCCAGC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%; Score 229.8; DB 7; Length 493; 93.4%; Pred. No. 6.3e-55; tive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Parchid Secretory Protein
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: Parotid Secretory Protein
                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/020,139
FILING DATE: 18 Dec-2001
CLASSIFICATION: <a href="https://doi.org/10.10mm/">doi.org/10.139</a>
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 15::
US-10-020-139-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-020-139-16; Sequence 16, Application US/10020139; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 301-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 493 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DUAN, ROXANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RUBEN, STEVEN
                         NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          842 TCCCAGTGGCTTGCCCC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AGCCAGTCTCTGTGCC 339
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O
                                                                                                                                                                                       IP: 20850
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Matches 240; Conserv
                                                                                                                                          STATE: MD
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
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797 GAAGAGGACGAATGAGGAGGACCACTGT-GGTGCTGCTGGTTGCTTCCC---AGTGGCT 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 CAGAAGGAGATATGTCCACTGATCCGCAT -- CTTCATCCACTCCCTGGATGTGAATGT -- 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            741 CATTCAGCAGGTCGT-CGATAATCCT-CAGCACAAAACCCAGCTGCAAACCC--TCATTT 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 GAAGANGACGAATGAGGANGACCACTGTGGTGCATGCTGATTGGTNTCCCAGTGGCTT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 TGCCCCACCCCTTATAGCATCTCCCTCCAGGAGCTGCTGCCA--CCACCTAACCAGGG 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AACAGCAGCTTCGAACAACATGNGGTTCTGGCCCCCGGGCAATAAAAGGCCCATTTTGGC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.5%; Score 129; DB 7; Length 395; Best Local Similarity 76.6%; Pred. No. 2e-26; Matches 279; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-10S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/020,139
FILING DATE: 18-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 301-8439
INFORMATION FOR SEQ ID NO: 16:
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,373
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER: PSECI ID NOS: 325720
SOFTWARRE: PSECISO FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 gtgaatgtcattcagcaggtcstcggtaa 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 733 GIGAAIGICATICAGCAGGICGICGATAA 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11687, Application US/10027632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                        77; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                             ; ORGANISM: Human
US-10-027-632-11685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-027-632-11687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-027-632-11687
                                                                                                                                                                      SEQ 1D NO 11686
                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                  CENGTH:
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APPLICATT: Wanstion.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLEOF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CACGAGATTTCATGAGCATCCTCTTAAACGCGTGTCAAGACAAAAGATGCTTCAGCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CACGANATTICATGAGCATCCTCTAAACACGTGTCAAAAAAAAAGATGCTTCAGGTT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TGGAAACTTGTTCTTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTTTT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TGGNAACTTGTTGTCCTATNCNGCGTGCTCACTGNGACCTCAGAATCTCTNCTT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.0%; Score 103.2; UB 7; Length 116; Best Local Similarity 92.1%; Pred. No. 2.7e-19; Matches 105; Conservative 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/020,139
FILING DATE: 18 Dec-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                       TITLE OF INVENTION: Parotid Secretory Protein
                                                                                                                      ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROOKES, ANDERS A.
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 301-8504
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-027-632-11686
; Sequence 11686, Application US/10027632
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
          APPLICANT: DUAN, ROXANNE
                                   STEVEN
                                                                           NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                           CITY: ROCKVILLE
                                     RUBEN,
                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                             20850
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                                                                                                                      673 TCCTCCCTGCTGCAGAAGAAGAAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTGGAT 732
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Debt of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.132
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.9%; Score 71; DB 7; Length 756; Best Local Similarity 86.5%; Pred. No. 6.3e-10; Matches 77; Conservative 1; Mismatches 11; Indels
6.9%; Score 71; DB 7; Length 756; 86.5%; Pred. No. 6.3e-10;
                                                           11; Indels
                                                              1; Mismatches
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1655 CURRENT APPLICATION NUMBER: US/10/176,912 CURRENT FILING DATE: 2002-06-20 Prior Application removed - See File Wrapper or Palm NUMBER OF SEC ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 SK., GBC., Y. BN. DS. HMKGTT.S., ..., YDSSNH. MKAMBTBM. SACH., M. NC. KB 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 ACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 780 MSARBYHT.S..T.WMB.KMT.YC.YRRHCSR.MMS.C.HTBGBAKHHY.KGNYTT.HYD 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720 ...NYNS.R.KC.T.HBK.M..A....DM.CA..YSR..RAD.HCRMK....BK.M...C.S 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 GCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATCAACC 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 TGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACTGATCCCCAGACACACC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600 SC., C.C., MC., NYH, BBH, MN., SBC, SD, A., TYYG, SMMT, RNBB, SH, 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       545 AGCCIGITGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 TGGACAAACACGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665 GCACTGTATCCTCCCTGCTGCAGAAGAGATATGTCCACTGATCCGCATCTTCATCCACT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 RCB. CH. MA. MKWY. HBNHSS.N. BABN. TBS.TC. AAST. W.SBTSWC. NKG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 SDTASNY.SB.A.S.TM.N.BC.SBA.CMHNDT.GS.BTK.A.C.BA.BC.SM... 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 SBC.SRNT.T...M..R.D.,TSAN..KBSCNC..HT.MB..SGNY..SRCH.C.BWS.. 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          785 AAACCCTCATTTGAAGAGGACGAATGAGGAGCACCACTGTGGTGCATGCTGATTGGTTCC 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        845 CAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAA 904
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.0%; Score 41; DB 7; Length 999; Best Local Similarity 7.9%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative 174; Mismatches 386; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 434, Application US/10179524 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
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                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 CCAGCGTG 912
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US-10-179-524-434/C
                                                                                                                                                                                                                                                                                                            US-10-176-912-434
                                                                                                                                                                                                 SEQ ID NO 434
                                                                                                                                                                                                                         LENGTH: 999
                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGCNCCGGGCCCATCATTGGGCCAGANTTATCAGAAGCCTCCNNGGANCTCCTG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.0%; Score 41.6; DB 7; Length 360;
Best Local Similarity 78.7%; Pred. No. 0.1;
Matches 59; Conservative 0; Mismatches 14; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                   TITLE OF INVENTION: Parotid Secretory Protein NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                    ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/020,139
FILING DATE: 18-Dec-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/993,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 301-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Sequence 434, Application US/10176912
// GENEFAL INFORMATION:
                                                     Sequence 18, Application US/10020139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 360 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
                                                                                                              APPLICANT: DUAN, ROXANNE
                                                                                                                                           STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                            CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 ACCGCAGTCACAATT 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ACCGCAGTCAACAAT 76
                                                                                                                                           RUBEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                       STATE: MU
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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  RESULT 13
US-10-020-139-18
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APPLICANT:
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APPLICANT: Wood William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C134
CURRENT APPLICATION NUMBER: US/10/179,524
CURRENT FILING DATE: 2002-06-24
Prior application removed - See File Wrapper or Palm
NUMBER OF SEO ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :| : :| : ::| : :::| : :::| : :::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 .SDTASNY.SB.A..S..TM.N..BC.SBA.CMHNDT.GS.BTK.A.C.BA.BC.SM... 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 ACAATGTCATTTCTAAGCTGCTTCCAACTAACACGGACATTTTTGGGTTGAAAATCAGCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 MSARBYHT.S..T.WMB.KMT.YC.YRRHCSR.MMS.C.HTBGBAKHHY.KGNYTT.HYD 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 ..NYNS.R.KC.T.HBK.M.A...DM.CA.YSR.RAD.HCRMK...BK.M.C.S 661
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                                                                                                                                                  Watanabe, Colin K.
Wood, William I.
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        Pan, James
Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-179-524-434
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LENGTH: 999
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Search completed: August 6, 2002, 18:20:30 Job time: 5264 sec

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Patent No. 5973119
GENERAL INFORMATION:
APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
FILE REFERENCE: A-524
CORRENT APPLICATION NUMBER: US/09/092,770
CORRENT FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 18
US-08-176-620A-5
US-08-461-985-5
US-08-451-985-5
US-08-932-7878-5
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US-08-932-012C-5
US-09-188-930-20
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US-09-004-838-21
US-09-004-838-21
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Best Local Similarity 25.9%
Matches 85; Conservative
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  ORGANISM: Human
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cyn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-252-851-8

US-09-222-851-7

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US-08-804-198-1

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US-08-804-198-1

US-08-804-198-1

US-08-804-198-1

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US-09-385-028-17

US-09-385-028-17

US-09-385-028-17

US-08-693-90-1

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US-08-693-90-90

US-08-693-694-5

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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Minimum DB Maximum DB

Searched:

Database :

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                                                                              APPLICANT: Dass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins FILE REFERENCE: A-524
CURRENT APPLICATION WUMBER: US/09/222,851
CURRENT FILING DATE: 1998-12-30
EARLIER FILING DATE: 1998-06-05
SEALLIER FILING DATE: 1998-06-05
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
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CURRENT APPLICATION NUMBER: US/09/092,770
CURRENT FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  539 CACACCAGCCTGTTGCCGTGGGAGA 566
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                        Sequence 8, Application US/09222851
Patent No. 6165753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.9%
Matches 85; Conservative
                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-09-222-851-8
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                     1215
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US-09-222-851-8
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Query Match 3.4%; Score 34.8; DB 2; Length 1214; Best Local Similarity 33.8%; Pred. No. 0.46; Matches 94; Conservative 32; Mismatches 152; Indels 0;
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33.8%; Pred. No. 0.46;
Live 32; Mismatches 152; Indels 0;
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APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Bobinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
FILE REFERENCE: A-524
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CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: 09/092,770
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 18
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; Patent No. 6165753
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Best Local Similarity 33.8%
Matches 94; Conservative
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                                                                                                                            APPLICANT: Halkier, Tychen
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
TITLE OF INVENTION: Methods of Using Thereof (As Amended)
TITLE OF INVENTION: Methods of Using Thereof (As Amended)
FILE REFERENCE: 4953.204-US
CURRENT APPLICATION WUMBER: US/09/295,186B
CURRENT FILING DATE: 1399-04-20
FRIOR PELING DATE: 1996-10-31
PRIOR FILING DATE: 1996-10-31
PRIOR FILING DATE: 1997-10-30
FRIOR FILING DATE: 1997-10-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASLSEQ for Windows Version 3.0
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APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TILE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                               Sequence 9, Application US/09295186B Patent No. 6127137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA (genomic)
ORGANISM: Hyphozyma sp. CBS 648.91
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                                                                                 GENERAL INFORMATION:
APPLICANT: Hasida, Miyoko
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NAME/KEY: mat_Peptide
; LOCATION: (442)...(1869)
US-09-295-186-9
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US-09-295-186-9
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Db 27325 TACACCCACGCCTGGAGATCGACGCCGAGGCCATCTTCGGCCCCGACTCACGCCAGGTG 27384
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                                                                                                                                                                                                                             US/08/804,227C
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,22
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORRENT AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INPORMATION FOR SEQ ID NO: 7:
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Kuhstoss, Stuart A.
Rao, Nagaraja R.
Richardson, Mark A.
Rosteck, Paul R., Jr.
                  STREET: LILLY CORPORATE CENTER CITY: INDIANAPOLIS
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                   : 44377 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                    Floppy disk
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36155..41830
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Matches 74; Conservative
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14046..20036
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31329..36071
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MEDIUM TYPE: Floppy of
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APPLICANT:
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                                                                           COUNTRY:
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us-10-020-139-1.rni

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Sequence 17, Application US/09385028 Patent No. 6232106
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                INFORMATION FOR SEQ 1D NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 942 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: unknown
 NUMBER OF SEQUENCES: 2
                     COMPUTER READABLE FORM:
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                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                              APPLICATION NUMBER:
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OPERATING SYSTEM:
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20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-385-028-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27265 GGCACCCTGCGGGCGGCCAGGCGCCCCCGCTGGCGGTGGCCTTCTGCCGCGCC 27324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               875 TCCCTCCAGGAAGCTGCTGCCACCACCACCAGGGTGAAAGCCTGAGTCCCACCAGAAG 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815 GGACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.3%; Score 33.8; DB 2; Length 44377; 52.5%; Pred. No. 8.2;
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 5869299el Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
           NUMBER OF SEQUENCES: 6
CORRESSONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                        US/08/804,198
                                                                                                                                                                                                                   Macintosh 7.0
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Patent No. 5869299
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                 SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804
                                                                                                                                                                                                                                                                                                                                                                36,470
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3865
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             935 GACCTTCCCAGATACCCCTTC 955
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                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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14046..20036
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31329..36071
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LOCATION: 350..14002
                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                            COMPUTER: Macintosh
OPERATING SYSTEM: Ma
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                                                                                     INDIANAPOLIS
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Best Local Similarity
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                                                                                                                          USA
                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                        46285
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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US-08-804-198-1
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                                                                                                                          COUNTRY:
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636 CCTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAAGGAGAT 695
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APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6223106
TITLE OF INVENTION: Acid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
3.3%; Score 33.6; DB 2; Length 942;
Best Local Similarity 53.9%; Pred. No. 0.95;
Matches 69; Conservative 0; Mismatches 59; Indels
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STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ): ORGANISM: Streptomyces clavuligerus

): STRAIN: Reisolate of S. clavuligerus ATCC 27064

US-08-446-806-2
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APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 33.6; DB 4; Length 942; Best Local Similarity 53.9%; Pred. No. 0.95; Matches 69; Conservative 0; Mismatches 59; Indels
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STREET: The Jeniler Buliding, 400 Seventh Street, N.W.
CITY: Washington
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPU)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
NAME: D. Douglas Price
REGISTRATION NUMBER: 24.514
REFERNCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-666
TELEPHONE: (202) 93905350
TELERA: (202) 93905350
TELERA: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1418/P57452US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEFAX: (202) 39305350
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                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                            LENGTH: 942 base pairs
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REGISTRATION NUMBER: 24
                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                  US-09-385-028-17
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3897 CATGAACATCGCGATCGACAACGCCAACCATCTCGGGCCTGCTGAAGGCCAACGC 3956
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                                                                                                                                                                                                                                                                                                                                                                                                            696 ATGTCCACTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGT 755
                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                          y Match 3.3%; Score 33.6; DB 4; Length 11604; Local Similarity 53.9%; Pred. No. 4.3; hes 69; Conservative 0; Mismatches 59; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TILE OF INVENTION: DNA Sequence Encoding Enzymes
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1418/P57452US2
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FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1416,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                               MOLECULE TYPE: DNA (genomic)
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                SEQUENCE CHARACTERISTICS:
LENGTH: 11604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 15079 base pairs
nucleic acid
EDNESS: single
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                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20004
                                                                                                                                                       US-09-385-028-13
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                                                                                                                TOPOLOGY:
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US-09-385-028-1
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                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                        Matches
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APPLICANT: Yee, Jing-Kuan
APPLICANT: Friedman, Theodore
APPLICANT: Friedman, Theodore
APPLICANT: Chen Shin-Tai
TITLE OF INVENTION: Inducible Expression System
TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                          5929 CATGAACATCGCGAYCGACACGCGCAACCATCTCTCGGGCCTGCTGAAGGCCAACGC 5988
                                                                                                                                                                                                              636 CGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGAT 695
                                                                                                                                                                                                                                                                                                   696 ATGICCACTGATCCGCATCTTCATCCACTCCTGGATGTGAATGTCATTCAGCAGGTCGT 755
                                                                                                                                                                         0; Gaps
                                                                                                                         3.3%; Score 33.6; DB 4; Length 15079; 53.9%; Pred. No. 5; tive 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,940
FILING DATE: 07-4UG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6510-055001
                                         ORGANISM: Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Bozicevic & Reed, LLP
285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08693940 Patent No. 6133027 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence
COTATION: 1...1953
(THER INFORMATION:
US-08-693-940.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
                                                                                                                       Query Match
Best Local Similarity 53.9%
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-327-340
TELEFAX: 650-327-3231
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z1P: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                      756 CGATAATC 763
HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                         US-09-385-028-1
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TITLE OF INVENTION: RECULATION OF SITE-SPECIFIC
TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC RECOMBINASE/NUCLEAR
TITLE OF INVENTION: RECEPTOR FUSION PROTEINS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         1681 GCCCAGCTCCTCCTCCTCCTCCCCACATCAGGCAATGAGTAACAAAGGCATGGAGCAT 1740
                                                                                                                                  1561 ACCCTGAAGTCTCTGGAAGAAGAACCATATCCACCGAGTCCTGGACAAGATCACAAGA 1620
                                               0; Gaps
                                                                                                                                                                            643 AGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCA 702
                                                                                                                                                                                                                                                                  703 CTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAAT 762
                                                                                       583 ACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAAT 642
    DB 3; Length 1956;
3.1%; Score 32.2; DB 3; Length 19
48.6%; Pred. No. 4;
tive 0; Mismatches 93; Indels
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LOCATION: (1-1269)
OTHER INFORMATION: /note= "FLP recombinase domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nikaido, Marmelstein, Murray & Oram STREET: 655 Fifteenth Street N.W. Suite 330
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02088
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08564264 Patent No. 6040430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Murray, Robert B. REGISTRATION NUMBER: 22,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PS. TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-JUN-1993
ATTORNEY/AGENT INFORMATION:
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Query Match
Best Local Similarity 48.64
Matches 88; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Tight Control of Gene Expression in
TITLE OF INVENTION: Eugaryotic Cells by Tetracycline-responsive Promoters
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                                                                                                                                                                                                                                                                                                                                                                                                        1927 ACCCTGAAGTCTCTGGAAGAGAAGGACCATATCCACGGAGTCCTGGACAAGATCACAGAC 1986
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                                                                                                                                                                                                                                                                                                                                                        583 ACCAGCATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAAT 642
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                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                  3.1%; Score 32.2; DB 3; Length 2322; 48.6%; Pred. No. 4.5; Live 0; Mismatches 93; Indels 0
                                                                                                NAME/KEY: misc_feature
LOCATION: (1285-2322)
OTHER INFORMATION: /note= "Estrogen binding domain."
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/076,726
FILING DATE: 14-JUN-1993
CLASSIFICATION: 435
                                                OTHER INFORMATION: /note= "Linker peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0942.2490001
TELECOMANICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       District of Columbia : United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08076726 Patent No. 5464758 GENERAL INFORMATION:
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NAME: ESENON, KODERT W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: both
NAME/KEY: misc_feature
LOCATION: (1270-1284)
                                                                                                                                                                                                                                                                             Best Local Similarity 48.6%
Matches 88; Conservative
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SOFTWARE: PatentI
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STATE: District of
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US-08-076-726-16
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1858 ACCCTGAAGTCTCTGGAAGAAGAACCATGTATCCACCGAGTCCTGGACAAGATCACAGAC 1917
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                                                                                      583 ACCAGCATCTCACTTTCCTTGCTGGACAACACAGGCCAAATCATCAACAAGTTCGTGAAT 642
                                                                                                                                                                           643 AGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCA 702
                                                                                                                                                                                                                                                               703 CTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAAT 762
                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bujard, Hermann
APPLICANT: Salfeld, Jochen
APPLICANT: Salfeld, Jochen
APPLICANT: Voss, Jeffred
TITLE OF INVENTION: Tight Control of Gene Expression in Bucaryotic
TITLE OF INVENTION: Cells by Tetracycline-responsive Promoters
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
3.1%; Score 32.2; DB 1; Length 4963; 48.6%; Pred. No. 7.1;
                                          0; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-013CP TELECOMMUNICATION:
TELEPHONE: (617) 227-5940
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Lext
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,452
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60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/08260452
; Patent No. 5650298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,32
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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                     Best Local Similarity 48.6
Matches 88; Conservative
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STRANDEDNESS: double
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APPLICANT: Gossen,
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  Query Match
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Query Match 3.1%; Score 32.2; DB 1; Length 4963; Best Local Similarity 48.6%; Pred. No. 7.1; Matches 88; Conservative 0; Mismatches 93; Indels 0; Gaps
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763 C 763 δλ 2038 C 2038

Search completed: August 6, 2002, 17:25:33 Job time: 4515 sec

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August 6, 2002, 16:49:58; Search time 66.51 Seconds (without alignments) 359.739 Million cell updates/sec
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1233
1 MLQLWKLVLLCGVLTGTSES......NVIQQVVDNPQHKTQLQTLI 249
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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283138

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	parotid secretory	י ערי	í va l	1)	mbrane	hypothetical prote	-0	010	0	dherence	in A - Clostri	_	kinesin-like spind	- 6	ace lave	DNA ligase (NAD+)	hypothetical profe	in - to		hypothetical prote	phosphoserine phos	thetical	nin-relat	tical pro	hetical prot	ole invasin	alvoornot	e membrane
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A64465	T30249	S77810	B82204	T19148	B89921	H89824	857596	T10094	D84999	T03754	H97217	S65186	S37854	A40305	T09649
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E C	fadsen,	H.O.	Hjorth,	J.P.	0	1	
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A;A	ccessi	con: A23	031 mRNA				
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A; R	itle: eferen	Coordin	ation o er: I53	f muri 236: M	ne J	parotid secretory protein an 87004556	nd salivary amylase expres
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Ō Ñ Ÿ	uery Mi est Lor atches	Query Match Best Local Similarity Matches 81: Conserv	29.6%; Solarity 33.8%; Pr	29.6 33.8	10 tb	Score 364.5; DB 1; Length Pred. No. 1.9e-19;	h 235;
δò	₩	MLQLWKI	LVELEGEVI	LTGTSES	SLLE	PVLHEGLE	n 09
g	7		:  :  VVLCGL	LIGNSES	SLLG	:      :                : ::  MFQLGSLVVLCGLLIGNSESLLGELGSAVNLKILNPF	: ::
Qy	61		KSSAWOL	AKOKAQE	SAEF	DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSI	LKISNSLILDVKAEPID 118
q <sub>0</sub>	49		QATSWPL/	AKNSILE	E	DVELLQQATSWPLAKNSILETLNTADLGNLKSFTSLNGLLLKINNLKVLDFQAKLSS	:   : : VLDFQAKLSS 105
Qy	119		LSFPVTA	NVTVAGE	DIId	DGKCLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDP	AVLGECASDP 178
qa	106		LTVPLAGE	EASLVLF	PFIG	NGNGIDLTVPLAGEASLVLPFIGKTVDISVSLDLINSLSIKTNAQTGLPEVTIGKCSSNT	: : : : VTIGKCSSNT 165

4

47; Gaps

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Fileasen, D.; Koehler, C.; Neuhaus, G.; Merkle, T.
Plant J. 201, 695-705, 1999
A:Title: Nuclear export of proteins in plants: AtxPol is the export receptor for leuc A; Reference number: 226149
A:Reference number: 226149
A:Residues: 1-1075 cHAA>
A:Residues: 1-1075 cHAA>
A:Residues: 1-1075 cHAA>
A:Residues: 1-1075 cHAA>
A:References: EMBL:Y18469; PIDN:CAB89280.1
A:Repertmental source: cultivar Columbia; 3wk-old green vegetative tissue C:Genetics:
A:Genetics:
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 16-Feb-2001
C:Accession: T52638
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                                                                                                                                                                                                                                                                                                                                                                                                                       57 KLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSL1LDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 IDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SPNGDEVTLKMPMALNASLSLPARDLTTDVSISMEAITSFAIEKDPKTGRRVLNMQRCSI, 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 DPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593 KIVQKCKRKEVIVQVGENEPFVSELLTGLATTVQDLEPHQIHSFYESVGNMIQAESDPQK 652
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                                                                                                                                                                                                                                                                                                        1 MFQLGSLVVLCGLLIGTSGSLFD1FQNPELDVESVWSE1NYR1RYALETMDLDMLADYLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KRGIE-------KIKDLRILNLNHEV 80
                                                                                                                                                                                         1 MLQLWKLVLLCGVLTGTSESLLDNLGN---DLSNVVDKLEPVLHEGLETVD-NTLKGILE 56
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            24.2%; Pred. No. 1.9e-08;
cive 53; Mismatches 85; Indels
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Best Local Similarity 23.8%; Pred. No. 4.5
                                                                                Conservative
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                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus
C.Species: Rattus norvegicus
C.Species: D.3 Peb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Aug-1999
C.Species: L.3 Ball, W.D.
J. R.Hirels, L.3 Rattus norvegicus
A.Feference number: A42337; MUID:92129360
A.Rocession: B42337
A.Roc
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Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A42337
R;Mirels, L.; Ball, W.D.
B;D.L. Chem. 257, 2679-2687, 1992
A;Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein az A;Reference number: A42337
A;Accession: 
179 TSISLSLLDKHSQ1INKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDN 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTN--TDIFG--LKISNSLILDVKAEP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 IDDGKGL/NLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 DPTSISLSLLDKKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVV 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%; Score 336.5; DB 2; Length 235; 31.8%; Pred. No. 2.1e-17;
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Best Local Similarity
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A; Reference number: $57357; MUID: 96090136
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A; Residues: 1-825 <KUR>
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                                                                                                            C.Accession: T51557
R.Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mewsubmitted to the Protein Sequence Database, August 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 33/3; 72/3; 103/3; 127/3; 163/3; 191/2; 237/3; 260/3; 286/3; 307/3; 322/3; 35
08/3; 954/3; 1000/3; 1035/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, February 1995
A.Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and A.Reference number: S53376
A.Reference number: S53376
A.Reference number: S53378
A.Reference number: S53278
A.Reference number: S63278
A.Residues: 1-1769
A.Residues: 1-1769
A.Residues: N.W.
Submitted to the Protein Sequence Database, September 1995
A.Reference number: S56876
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A. Cross-references: EMBL: 249384; NID:91008292; PID:91008293; MIPS:YJL109c
R. Rasmussen, S. W.
Feast 11, 873-883, 1995
A. Title: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3.
           Exportin1 (XPO1) protein - Arabidopsis thaliana (fragment)
Alternate names: protein F2K13_170
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug_2000 #sequence_revision 18-Aug-2000 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable membrane protein YJL109c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J0808
C;Species: Saccharomyces cerevisiae
C;Date: 05:May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S53378; S56887; S57359
R;Rasmussen, S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.0%; Score 110.5; DB 2; Length 1075; Best Local Similarity 23.8%; Pred. No. 4.5; Matches 68; Conservative 46; Mismatches 107; Indels 65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593 KIVQKCKRKFVIVQVGENEPFVSELLTGLATTVQDLEPHQIHSFYESVGNMIQAESDPQK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VDLGVLQKSSA-----W-QLAKQKAQEAEKLLNNVISK----LLPTNTD-----IFGLK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 ISNSLILDVKAEPIDDGKGLNL----SFPVTANVTVAGPIIGQ--IINLKASLDLLTAVT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 IET -- DPQTHQP-------VAVLGECASD-PTSISLSLLDKHSQIINKFVNSVINT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    762 IETFLDKAEDQPHICKQFVPPMMESVLGDYARNVPDARESEVLSLFATIINKYKATMLDD 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 KLVLLCG----VLTGTSESLLDNLGNDLSNVYDKLEP-VLHEGLETVDNTLKGILEKLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 LKSTVSSLLOKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI 249
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                                                                                                                                                                                                                                                                                                                                                          Experimental source: cultivar Columbia; BAC clone F2K13
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C;Superfamily: Arabidopsis thaliana exportin 1
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A; Residues: 1-1075 <SAT>
A; Cross references: EMBL AL391141
A; Experimental source: colliner
                                                                                                                                                                                                Reference number: 225394
Accession: T51557
                                                                                                                                                                                                                         A;Accession: T51557
A;Status: preliminary
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A; Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-1769 <RAF>
A;Cross-references: EMBL:X85021; N1D:g728698; P!DN:CAA59385.1; PID:g728701
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 SILTFLDKEDKPVCDKFITSYTRSIARYDRS-----KLNIILSLLKK-----IRLERY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 EAEKLLNNVI--SKLLPTNTDI-----FGLKISNSLILDVKAEPIDDGKGLNLSFPVTAN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 EVRLIITULIYLSEILEDKSQLVELFEYFISINEDLVLKCL-----KSLGLT----- 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 VTVAGPIIGQIINLKASLDLLTAVTIETD--PQTHQPVAVLGECASDPTSISLSLLDKHS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 ------GELFEIRLTTSLFTNADVNTDIVKQLSDPV----ETTKKDTASFQTFLDKHS 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 SLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQ 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 19.2%; Pred. No. 11; Matches 52; Conservative
A;Accession: S57359
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Matches 72; Conservative 39; Mismatches 94; Indels
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C:Keywords: transmembrane protein
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Db 194 QLIYDIKGIGFNKADQLARNIGIAYNDNERLKAALLYTLEEECIKOG 240	Matches 50; Conservative 31; Mismatches 64; Indels 48; Gaps 9;
Oy 163 QTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 216	Qy 52 KGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSI.HJ) 111   1   1   1   1   1   1   1   1
OY 217 CPLIRIFIHSLDVNVIQQVVDNPQHKTOLQTLL 249	QY 112 VKAEPIDDGKGLNLSFPVTANVFVAGPIIGQIINLKASLD 151 
RESULT 8	Qy 152LLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQ11NKF 196   ::
probable ligand-binding protein RYA3 - rat C:Species: Rattus norvegicus (Norway rat) C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C:Accession: S17448 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999	197 VNSVINTLKSTVS 209 11:1:   1   261 SRALVSDLNAQQS 273
regions of the olfactor	RESULT 10 T50073
27730	myosin-like coiled-coil protein sp8 [imported] - fission yeast (Schizosaccharomyces p. C.Species: Schizosaccharomyces pombe C.Species: Schizosaccharomyces pombe C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000 C. C. Coccesion: T50073
	Avecassion: TSO073 A:Status: preliminary; translated from GB/EMBL/DDBJ
MIQLWKLVLCGVI,TGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILE 56	A.MOLECULE TYPE: UNA A.Residues: 1-1727 < MCD> A.Cross-references: EMBL:AL133357; PIDN:CAB62414.1; GSPDB:GN00066; SPDB:SPAC1486.04c A.Rxperimental source: strain 972h(-); cosmid c1486
112	A;Gene: SPDB:SPAC1486.04c A;Map position: 1
	Query Match 8.5%; Score 104.5; DB 2; Length 1727; Best Local Similarity 24.3%; Pred. No. 23; Matches 63; Conservative 41; Mismatches 94; Indels 61; Gaps 11;
	QY 18 SESLLDNLGNDLSNVVDKLEPV
QY         203        TLKSTVSSLLQKEJCPLERIFIHSLDVNVIQQVVDNPQ         240           :::  :::	Qy 50TLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIF 100   :     :     :
RESULT 9 849943	QY 101 G.KISNSLILDVRAEPIDDGKGLNLSF·PVTANVTVAGPIIGQIINLKASLDLLTAVTIE 159 
fructose-bisphosphate aldolase (EC 4.1.2.13) · Staphylococcus carnosus (strain TM300) s; Species: Staphylococcus carnosus carnosus carnosus and in Nov-1994 #sequence_revision 11-Nov-1994 #text_change 15-Oct-1999 cassion: A49943; S33358	OY 160 TDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPL 219  bb 508 NVPATVQVALDEYAQNPSTASETLVNKELANFSSIKEAVSKTLE 551
<pre>A;Witke, C.; Goetz, F. J. Bacteriol. 175, 7495-7499, 1993 A;Title: Cloning, sequencing, and characterization of the gene encoding the class I fructive ference numbers. A49943; MUID:94042930</pre>	QY 220 IRIFIHSLDVNVIQQVV 236 :  ::        :      Db 552 LREKVRALECDVEIQKQTV 570
A:Status: preliminary A:Koteoule type: DNA A:Roleoule type: DNA A:Residues: 1-296 <wit> A:Cross-references: BRBL:X71729; NID:9297873; PIDN:CAA50663.1; PID:9297874 C:Keywords: aldehyde-lyase; carbon-carbon lyase</wit>	RESULT 11 G64242 Gytadherence-accessory protein (hmwl) homolog MG386 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text change 07-Dec-1999
Query Match Query Match Best Local Similarity 25.9%; Pred. No. 1.8;	C:Accession: G64342 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R. M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Werrick, , C.A.; Venter, J.C.

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ArTitle: Comparative sequence analysis of the Clostridium difficile toxins A and B. ArReference number: S22434; MUID:92293124
A.Accession: S22437
                                                                                                                                                                                                                          A:Note: the four tragments shown in reference A60991 correspond to four types of red with repeats ordered ABCCCDABCDDABCCCDABCCDABCDABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     984 STSVKVQLY---AQLFSTGLNTIYDSIQLVN----LISNAVNDTINVLPTITEGI----- 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807 KTLLLDASVSPOTKFILMNLKLNIESSIGDYIYYEKLEPVKNIIHNSIDDLIDEFNLLEN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867 VSDELYELKKLNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Mismatches 109; Indels 48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 ----LKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 TIETDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEI 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KLVLLCGVLTGTSESLLDNJGNDLSNVV-----DKLEPVLHEGLETVDNTLK--GILEK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Gene: toxA

S:Superfamily: Clostridium difficile toxin A: cpl repeat homology
C;Keywords: cytotoxin; enterotoxin
F;1820-1839/Domain: cpl repeat homology <CPOl>
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                                                                                                                                                                                                                                                                                                                                                                                                        A Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-55, 'V', 57-2079, 'L', 2081-2549, 'S', 2551-2710 <SAU>
                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 18, 1629-1630, 1990
A;Title: Nuclectide sequence of Clostridium difficile toxin A.
A;Reference number: S08637; MUID:90221894
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20.3%; Pred. No. 45
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Nucleic Acids Res. 18, 1629-1630, 199
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                                              Gen. Genet. 233, 260-268, 1992
                                                                                                                                                                           A.Residues: 1-92 <VON>
A.Cross-references: EMBL:X60984
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C.Genetics:
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F.1861-1881/Domain: cpl re
F.1933-1952/Domain: cpl re
F.1953-1973/Domain: cpl re
F.1954-1994/Domain: cpl re
F.1995-2015/Domain: cpl re
F.2067-2086/Domain: cpl re
F.2087-2107/Domain: cpl re
F.2108-2128/Domain: cpl re
F.221-224/Domain: cpl re
F.221-224/Domain: cpl re
F.2315-2334/Domain: cpl re
F.235-2376/Domain: cpl re
F.235-2376/Domain: cpl re
F.235-2376/Domain: cpl re
F.235-2376/Domain: cpl re
                                                                                                                                                     A: Molecule type: DNA
A: Residues: 1-92 <VON>
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F;2673-2694/Domain:
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R:Dove, C.H.; Wang, S.Z.; Price, S.B.; Phelps, C.J.; Lyerly, D.M.; Wilkins, T.D.; Johnsq A; Title: Molecular characterization of the Clostridium difficile toxin A gene.
A; Reference number: A37052; MUID:90129305
A; Accession: A37052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Residues: 1-2710 cbov>
A:Cross-references: 6B:M30307; NID:g144925; PIDN:AAA23283.1; PID:g144926
R:Wren, B.W.; Clayton, C.L.; Tabagchali, S.
Brims Microbiol. Lett. 70, 1-6, 1990
A:Title: Nucleotide sequence of Clostridium difficile toxin A gene fragment and detection and detection
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R:von Eichel-Streiber, C.; Laufenberg-Feldmann, R.; Sartingen, S.; Schulze, J.; Sauerbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :Molecule type: DNA
:Residues: 'I',1894-1899,'K',1901-1910,'Y',1912-1919;2054-2074;2096-2116;2138-2158 <WRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laufenberg-Feldmann, R.; Sartingen, S.; Schulze, J.; Sauerborn,
                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1616 <FIGR>
A;Residues: 1-1616 <FIGR>
A;Cross-references: GB:U39723; GB:L43967; N1D:q1046092; P1D:g1046097; TIGR:MG386
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                             A; Accession: 664242
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 SKEIKUSARADLSNISDDIDSVWKEFGSFTDETCKSVEEKSQVDEILLDANNDF---INE 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Clostridium difficile
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 24-Sep-1999
C;Accession: A37052; A60991; S21897; S22437; S08638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 --IFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVA-----GPIIGQ1--IN---- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 TALFSEKLVNEVLL--TNEYVD----VNAPFSTETEVKVSSELPKSELVDEITFINNDPK 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 ----LKASLDLL------TAVTIETDPQTHQPVAVL-----GECASDPTSI 181
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 POEGLEYKVDFLETEPKSLFDEKTTIVVESEPPFIQPDLSLELDSVNDVDKSLETKTTSV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 SESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQK 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 ----- KLLPTNTD----- 98
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 23;
48; Mismatches 75; Indels 120;
                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1616;
Science $70, 397-403, 1995
A:Tille: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200: MUID:96026346
A:Accession: G64242
                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 104;
20.6%; Pred. No. 2
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Matches 63; Conservative
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A: Pasidues: 1-154 <EIC>
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RESULT 13	Db 447 LDQCKSDLQNKTQELE
hypothetical protein SA2399 [imported] - Staphylococcus aureus (strain N315)	Qy 80 E-AEKLLNNVISKLLPTNTD
C.Date: Johny-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C.Accession: F90067	Db 494 DAASKLLNTVEETTKD
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	Qy 128PUTANVŢVAGPIIGO   :   :     Db 550 KDGSSKQKAMLEVHKŢLFGN
ArTitle: 757, 1223-1240, 2001 ArTitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A.Reference number: A89738; MUID:21311952; PMID:11418146 A:Accession: F90067	QY 182 SLSLLDKHSQIINKF Db 507 STHVSOLENHIEFOR
A;Status: preliminary A;Status: DNA A;Molecule type: DNA A;Residues: 1-306, emins.	221
A. Nesidues: 1-29 KNUK. A. Cross-reterences: GB:BA000018; P1D:g13702563; PIDN:BAB43704.1; GSPDB:GN00149 A. Experimental source: strain N315 C:Genetics: A. Gene: SA2399	Db 653 QLKHIFKTSLTVADKIEDQKI
Query Match Best Local Similarity 25.5%; Pred. No. 2.7; Matches 53; Conservative 30; Mismatches 68; Indels 57; Gaps 10;	
LNNVISKLLPTN-TD1 99 :: :	Ryanonymous, The Xylella fastic Nature 406, 151-157, 2000 A'Title: The genome sequence or
Oy 100 FGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIIN	A. Note: for a complete list of A. Accession: C82759 A. Strus: preliminary A. Scholonic tron.
Qy 146LKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISL	A.Corecate Cype: UNA A.Residues: 1-990 CSIM> A.Cross-references: GB:AE003921 A.Experimental source: strain
	F.C. Bringbon, A.J.G.; Reladon, F.C. Briones, M.R.S.; Bueno, M.R.P.; as-Neto, E.; Docena, C.; El-Dorsubmitted to GenBank, June 2000
TAC PREEDING WELL TOOK ON THE WAS DEPARTED ON	A; Authors: Ferreira, V.C.A.; Fe J.D.; Jungueira, M.L.; Kemper, chado. M.A. Madaira, M.N.
<pre>RESULT 14 G02157 Kinesin-like spindle protein HKSP - human C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001 C;Accession: G02157 R;Whitehead, C. Submitted to the EMBL Data Library, September 1995</pre>	A.Authors: Martins, E.M.F.; Martins, M.J.; Martins, M.J.; de M. A.Authors: da Silva, A.C.R.; da M.J.; Tsuhako, M.H.; Vallada, H.; A.Reference number: A59328
A;Reference number: H00839 A;Accession: G02157 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA	ý
A:Residues: 1-1056 <whi> A:Crost-references: EMBL:037426; NID:g1171152; PIDN:AAA86132.1; PID:g1171153 C:Genetics:</whi>	Query Match 8.1% Best Local Similarity 21.3% Matches 54; Conservative
A;Gene: GDB:KNSL1; Eg5; KSP A;Cross-references: GDB:132856; OMIN:148760 A;Map position: 10q24.1-10q24.1 C;Superfamily: kinesin-related profeto EdS: kinesis mass:	Qy 15 TGTSESLLDNLGNDLSNVVDK :     : :     : : Db 706 SGTNEAIQSLTATDLKDFQQR
C:Keywords: ATP; nucleotide binding; P-loop F:19-365/Domain: Kinesin motor domain homology <kmot> F:105-112/Region: nucleotide-binding motif A (P-loop)</kmot>	Oy 74 AKQKAQEAEKLLNNVISKLLP 
Query Match 8.2%; Score 100.5; DB 1; Length 1056; Best Local Similarity 23.0%; Pred. No. 24; Matches 65; Conservative 39; Mismatches 89; Indels 89; Gans 14.	OY 133 VTVACPIIGOIINLKASLDL- i   : :::  Db 810 INVGNEAEGGTFSSRLNMNLR

89; Indels 89; Gaps

22 LDNEGNDLSNVVDKLEPVLHEGLETVDNTLKG1LEKLKVDLGVLQK--SSAWQLAKQKAQ 79

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ELL; Kitajima J.P.; Franca, S.C.; Franco, M.C.; Fr
B.L.; Kitajima J.P.; Krieger, J.E.; Kuramae, E.E.; Le
Madelra, H.M.F.; Marino, C.L.; Marques, M.V.; Martine,
Leukuma, A.T.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
de Rosa Jir., V.E.; de Sa, R.C.; Santelli, R.V.; Save
Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva,
Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrerry, H.; Facincani, A.P.; Ferreira, A.J.S.
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"LFGI,--KISNSLILDVKAEPIDD--GKGLNLSF----- 127
                                                                                                                                           VSGLHSKLDRKKAVDQHNAEAQDIFGKNLNSLFNNMEEL1 549
                                                                                                                                                                                                IINLKAS-LDLLTAVTIETDPQTHQPVAVLGECASDFTSI 181
                                                                                                                                                                                                                                     -----VNSVINTLKSTVSSLLQKEICPLI----- 220
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ID:20365717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed] - Xylella fastidiosa (strain 9a5c)
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235 VVDNPQHKTQLQTL 248 :| :| :| 11| 916 IVRYERPDNYIQTL 929 Ωy

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Search completed: August 6, 2002, 17:05:10 Job time: 912 scc

AX061621 Sequence AF432917 Homo sapi AL121901 Human DNA U79413 Bos taurus U79414 Bos taurus

AK024183 Homo sapi AJ006614 Homo sapi Continuation (6 of AC005800 Homo sapi CONTINUATION (5 of AC002312 Human Chr AC094795 Rattus no AL137059 Human DNA AC097610 Rattus no AP001854 Homo sapi AC067966 Homo sapi AC106518 Rattus no AC106518 Rattus no

Perfect score: Sequence: Scoring table:

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AL392047 Human DNA
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AC109187 Mus muscu
AC003815 Cryza sat
AP002091 Homo sapi
AC008560 Homo sapi
AC012031 Homo sapi
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U88974 Streptococc AC102174 Mus muscu Homo sapi Rattus no Homo sapi Homo sapi Homo sapi Homo sapi

Score

Result

Canis fam

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7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	200

Query Match 100.0%; Score 746; DB 6; Length 1058; Best Local Similarity 100.0%; Pred. No. 0; Matches 746; Conservative 0; Mismatches 0; Indels 0; Ga 1 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTC 1	Qy         61 TCTTCTTGACAATCTTGGCAATGACCTAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120           IllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         241 AGCTGAGAAATTGCTGAACAATGTCAATTCTAAGCTGCTTCCAACTAACACGGACATTTT         300	0y         421 TGGCCAGATTATCAACCTGAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAAC         480           111111111111111111111111111111111111	0y         601 GATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCAGAGGACATATGTCCACTGAT         60           bb         666 GATCAACACGCTGAAAGCACTGTATCCTCCCTGCTGCAGAGGAGATATGTCCACTGAT         725           Qy         661 CCGCATCTTCATCCACTCCTGGATGTGCATGCTCGAGGAGATATCTCACTCA	RESULT 2 AF432917 LOCUS LOCUS LOCUS LOCUS LOCUS HOMO Sapiens parotid secretory protein mRNA, complete cds. ACCESSION AF432917.1 G1:16755849 KEYWORDS COURCE HOMAD: ORGANISM REPERENCE REPERENCE AUTHORS AUTHORS AUTHORS AUTHORS A member of the PSF/plunc family of BPI proteins is expressed in the human parotid gland
8 2.4 165949 2 AC068029 8 2.4 163243 9 AL513304 8 2.4 163996 2 AC053501 8 2.4 164916 9 AC011224 8 2.4 165176 9 AC078941 8 2.4 165736 9 HSSP15 8 2.4 167336 2 AC021350 8 2.4 167639 2 AC057815	67939 9 AC008014 AC008014 67008014 67008014 67008 6873 9 AL3546063 AL3546063 AL3546063 6873 9 AL3546083 AC007172 68616 2 AC007172 AC013636 AC013636 AC013636 AC013636 AC01363 AC01363 AC01363 AC01363 AC01363 AC01363 AC01363 AC026989 AC026989 AC026986 AC020562 AC0205	8 2.4 172663 5 ACU33406 8 2.4 173028 9 ACU93376 8 2.4 173524 9 ACU90371 8 2.4 17372 2 AL450993 8 2.4 174128 2 APD01123 8 2.4 174189 9 ACO68185 8 2.4 17414 3 ACU11066 8 2.4 175071 2 AC01274 8 2.4 175072 2 AC027254	### ALCONMENTS  ###################################	Eukaryota: Metazoa; Chordata; Craniata; Eukaryota: Metazoa; Chordata; Craniata; Mammalia: Eutheria: Primates; Catarrhin E 1 (bases 1 to 1038) S dumas milne Edwards, J.B., Bougueleret, L Complementary dna's encoding proteins w L Patent: WO 0100806-A 26 04-JAN-2001; GENSET (FR) Location/Qualifiers 1. 1058 //organism="Homo sapiens" //db_xref="taxon:9606" //db_xref="taxon:9606"	/note="unnamed protein product" /codon_start= /codon_start= /codon_start= /codon_start= /codon_start= /codon_start= /d="CAC4982.1" /db_xref="G1:12406704" /translation="MQDWALVLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL ETVONTLKGILEKLKVDLGVLGKSAMQLAKGAEKLLNNVISKLLPTNTDIFGL KISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIGGIINLKASJDLTAVTIET DPQTHQPVANLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP LIRFIHESLDVNVIQQVVDNPQHKTQLQTLI"  polyA_signal

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DPQTHQPVAVLRCASDPTSISLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
LIRIFIHSLDVNVIQQVVDNDQHKTQLQTLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 ATCTCACTTTCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CITCITGACAATCTIGGCAATGACCIAAGCAATGICGIGGATAAGCIGGAACCIGITCIT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 CACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGTC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACAGGGACATTTTT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 AAAGGCCTTAACCTGAGCTTCCCTGTCACGGGAATGTCACTGTGGCCCGGGCCCATCATT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 GGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAACT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ATGCTTCAGCTTTGGAAACTTGTTCTCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCT 61
                                                        Submitted (12-oct-2001) Molecular, Cellular and Craniofacial Biology, University of Louisville, 501 S. Preston Street, Louisville, KY 40992, USA Louisville, KY 40992, USA
                                                                                                                                                                                                                                     /note="salivary protein; putative BPI protein; PSP; similar to BSP30 and plunc/lunx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.0%; Score 694; DB
99.9%; Pred. No. 0;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    176 t
                                                                                                                                        /organism="Homo sapiens"
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             2 (bases 1 to 750)
Venkatesh,S.G. and Gorr,S.-U.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                 163 g
                                                                                                                                                                          /chromosome="20"
                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                         /sex-"male
                                                                                                                                                                                                                                                                                                                                                                                                                  210 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744; Conservative
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 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
Matches 74
                                                                                                                           SOUTOR
                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                           TITLE
JOURNAL
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               REFERENCE
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROY; Tr.; TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/ChrO of the Sanger Centre insert of clone RP1149/ChrO of the Sanger of the sanger can the sequence. The true left end of clone RP1149G10 is at 1 in this sequence. The true left end of clone RP5-11874 is at 161494 in this sequence. The true left end of clone RP5-11874 is at 161494 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with a leternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-49G10 is from the library RPC1-111.1 constructed by the group herror, over harmony was heart of the sequence of the phasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSBA49G10
HSBA49G10
HUman DNA sequence from clone RPI1-49G10 on chromosome 20 Contains a gene similar to bovine salivary protein BSP30,the LoC51297 gene for LNX protein, 5 end of a gene encoding a protein similar to murine von ebner minor salivary gland protein, a novel gene, a pseudogene similar to STAT-induced STAT inhibitor. 2, a pseudogene similar to ribosomal protein L12, a putative novel transcript, ESTS, STSS, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 5, 2000 this sequence version replaced gi:8017404.
                                         662 CUCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAG 721
                                                                                                                                                                                                                                              661 CCCATCTTCATCCACTCCCTGGATGTGATGTCATTCAGCAGGTCGTCGATAATCCTCAG 720
602 ATCAACACGCFGAAAAGCACTGFATCCFCCCFGCTGCAGAAGGAGATAFGTCCACFGATC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; BSP30; CpG island; LOC51297; LUNX; RPL12; STAT-inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                722 CACAAAACCCAGCTGCAAACCCTCA 746
                                                                                                                                                                                                                                                                                                                                                                                   AL121901.20 GI:8249854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .161593
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/db\_xref="taxon:9606"

.48787)

48600.

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35525. .48787
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KISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match: proteins: Tr:095102 Tr:088582 Tr:014542 Tr:014509
Tr:062225 Tr:015097 Tr:035718 Tr:090x77 Tr:090x78
Tr:070512 Tr:035960 Tr:09PW70 Tr:09Y5R1
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                                                                                                                                                                                                                                              /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"bA49G10.2"
/note-"bA49G10.2 (similar to STAT-induced STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 161593;
                                                                                                                                                                                                      /note="match: proteins: Tr:P79125 Sw:P07743"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.3%; Score 159; DB 9; 1
100.0%; Pred. No. 7.8e-82;
                                                                                                                                                                                                                                                                                                                                                                                                             LIRIFIHSLDVNVIQQVVDNPQHKTQLQTLI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (53844.
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                                                                                                                 gene
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                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Tandem repeat. Forced join. Approximately 500 bases missing according to restriction digest." 16387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="56 copies 2 mer ct 63% conserved"
33693. .33762
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33733. .33785
/note="MER47 repeat: matches 1. .55 of consensus"
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/note="match: GSS: Em:AQ339300"
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/note="41 copies 2 mer ag 75% conserved"
complement(21172. .21428)
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                                                                                                                                                                                                                                      613 .678
/note="33 copies 2 mer ca 75% conserved"
                                                                                                                                                                                                                                                                                                                 3140. .5183
/note="22 copies 2 mer tt 75% conserved"
                                                                                                                                                                                /note="37 copies 2 mer ca 66% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AZ102442"
20999. .21238
/note="4 copies 60 mer 69% conserved"
21031. .21263
                                                                                                                                                                                                                      copies 77 mer 83% conserved"
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complement(8476. .902)
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complement(14766. .15061)
14772. .14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11882. .32061
note="3 copies 60 mer 73% conserved"
11921. .32032
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complement(1. .107)
/note="match: GSS: Em:AQ607627"
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/note="match: GSS: Em:AQ550113"
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/note="match: GSS: Em:AQ727877"
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26979. .27422
/note="match: GSS: Em:AQ636646"
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/chromosome="20"
/clone="RP11-49G10"
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DSTIBLIFQNLKTELESRCLMDVVEFTQQTENSLEGLISRIFQVVNKLTGVRIRNVQV
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VVVGECPNNFESISTTYLHRRRGLLMDVVDFGVNLVRQLVSSVVQHELCPRIRELLES
LDTECIKKLIGEPQVTTQQESEVHR"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Pecora; Bovoidea
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Haigh.B.J., Wilkins,R.J. and Wheelet.....
Direct Submission
Submitted (21-NoV-1996) Dairy Science Group, AgResearch, Private Bag, Hamilton, New Zealand
Localion/Qualifiers
                                                        36521 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTC 36580
                                                                                                                                                Db 36581 TCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTGGTGGATAAGCTGGAGCACCTGTTCT 36640
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Bos taurus common salivary protein BSP30 mRNA, form b, complete
                                                                                                            61 TCTTCTTGACAATCTTGGCAATGACCTAAGGAATGTCGTGGATAAGCTGGAACCTGTTCT 120
                                    1 GATGCTTCAGCTTTGGAAACTTGTTCTGCTGTGCGGCGTGCTCAGTGGGACCTCAGAGTC 60
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Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
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/db_xref="GI:1710367"
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100.0%; Piv
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Matches 23; Conservative
Matches 159; Conservative
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/translation="WYOLMSULLEGILAGTSASLPDIRGNDVLRKIKSGLERGLDTFDSTIEGNIKTELESRCSDEVVEOUETBRELEGILSRIFOVVSKLTGVB.RRVOVPDITFEATSENSANVLIPITADVTVSLPFLGEIVDLDLAVVDLGTTVSIETDTEDPQVVVGETNRPESISLTVLHGSRFGLVNDVVDIGVNLARRVVSSVVEGELCPRFRELLESLDAGEVEVKLIGESOTTOOPPEGER 230 t 251 c 251 c 254 q 230 t
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                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                  The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parotid Secretory Protein family Unpublished
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1 (Sites)
1 (Sodair T. Ota, T. Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takahashi, M., Chiba, Y., Ishida, S., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        Submitted (21-NOV-1996) Dairy Science Group, AgResearch, Private Bag, Hamilton, New Zealand Location/Qualifiers
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Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMAl
clone:MAMMA1002009.
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                                                                                 Bovidae; Bovinae; Bos.
1 (bases 1 to 1024)
Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
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Haigh,B.J., Wilkins,R.J. and Wheeler,T.T.
Direct Submission
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/db_xref="G1:1710369"
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Best Local Similarity 100.
Matches 23; Conservative
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Bos taurus
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Pred. No. 2.2;

100.08;

Best Local Similarity

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Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
Tel:81-438-52-3951, Fax:81 438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5. a 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ^{\prime} 9043 bp DNA linear PRI 17-NOV-2000 Homo sapiens chromosome 18 sequence from PAC RPCI-1 34\,E09 , complete sequence.
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/clone="PAC RPCI-1 34E08"
/clone="PAC RPCI1.3-5 Human PAC library, originating
instute: Roswell Park Cancer Institute, creator: Pieter
de Jong, P. Ioannou"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (17-JUL-1998) MPIMG, Abt.Lehrach, Max Planck Institut
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Radelof, U., Henniq, S., Ramser, J., Francis, F., Steffens, C., Klein, M., Seranski, P., Poustka, A., Reinhardt, R. and Lehrach, H. Unpublished
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On Nov 19, 2000 this sequence version replaced gi:9931108.
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iive 0; Mismatches 0; Indels
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/note="cloning vector: pME18SFL3"
358 c 383 g 442 t
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/db_xref*"taxon:9606"
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                                                                                                                                                                                                          University of Tokyo.
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2.8%; Score 21; DB 9; Length 79043;

Query Match

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Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
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/rpt_family."Alu" repeat_region complement(2247123679) /rpt_family."Alu" repeat_region complement(2409624132) /rpt_family."MrF repeat_region complement(2449924512)	<pre>/rpt_family="Alu" complement(24555. /rpt_family="Alu"</pre>	2553125825 /rpt_family~"Alu"	complement(26649. /rpt_family="LTR12	repear_region   Comprement(211523403)   /rpt_family='Alu   reneat region   comprement(36436 30780)	/rpt_family-"M1R" 2984530134	/rpt_family="Alu" repeat_region 3120531310	/ipt_region 31639318195 /repeat_region 3163931819.	repeat_region 3197	repeat_region complement(3730837597)	repeat_region 39733 39975	repeat_region 41460. 4174.	repeat_region //rel_raminj riu //relion //rel //	repeat_region 45731 .4602 /rpt_family="Alu"	repeat_region complement(46882, .47170)	repeat_region 4738047485 /rpt_family="Alu"	repeat_region 47588, 47689 /rpt family="Alu"	repeat_region complement(47697, .47893)	repeat_region complement (4799) .48102)	repeat_region 48285 .48932 /rpt_family-"Alu"	complement(50231/rpt_family*"Alu"	complement (50621 /rpt_family="Alu"	<pre>complement(51343 /rpt_family="Alu"</pre>	<pre>complement(52253 /rpt_family*"Alu"</pre>	repeat_region complement(5272353003) /rpt_family="Alu"	repeat_region complement(54243. 54702)	repeat_region complement(5.55271)	repeat_region 599896020	repeat_region complement(6026044)	repeat_region 612061310.	repeat_region 61475. 61770 /rpt_family="Alu"
Dal 8,	repeat_region complement(201798) repeat_region complement(9981296)	/rpt_tamily~"Alu" repeat_region complement(2600, .2728)	repeat_region /1pc_remily= Alu /1pc_region /1pc_family= Alu	repeat_region complement(36403919) /rpt_family="Alu"	40664343 /rpt_family="Alu"	repear_region / rpt_family="Alu" repear_region 53405256		<ul> <li>repeat_region complement(70257320)</li> </ul>	/rpt_family="Alu" 77948574	/rpt_family="Alu" repeat_region 9342, .9628				/rpt_tamily="Alu" repeat_region 11219, .11614	/rpt_family="Alu" repeat_region 12005, 12278	/rpt_tamily="Alu" repeat_region complement(1270212975)	/rpt_family="Alu" repeat_region 13977, .14253	/rpt_family="Alu" repeat_region 1530215579	/rpt_family="Alu" repeat_region 16461, .16754	repeat_region 17368	repeat_region complement[18436)	repeat_region 18671 stu /ror family="halv"	repeat_region 18693. 119989 /rot family="blum"	repeat_region 1980	/rpt_ramlly="ALU" repeat_region 19740. 20131	/rpt_family="Alu" /rpt_family="Alu" repeat_region complement(2036920457)	/rpt_family="Alu" repeat_region 2105821203	/rpt_family="Alu"	/rpt_family="Alu" .repeat_region complement(2175222309)	/rpt_family="Alu" repeat_region complement(2237123005)

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Nuzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adass, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adams, C., Adams, C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burea, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C., Burett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carten, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, S., Chochty, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederict, D.A., Delaney, K.R., Davigac, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Dulhin, K.J., Earnhart, C., Edgar, D., Edvards, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Glill, R., Gorrell, J.H., Gaovara, W., Gunaratne, P., Hanes, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Johnson, R., Jolivet, S., Joudah, S., Kallson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Louis, L., Li, J., Li, Z., Lichtarge, O., Liu, J., Liu, R., Luna, R., Luna
Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T. and Wilson, R.

Direct Submission

Submitted (09-Jul-1997) Genome Science and Technology Center,
University of Texas Southwestern Medical Center at Dallas, 5323

Harry Hines Blvd, Dallas, TX 75235-8591, USA

E Vans, G.A., Athanasiou, M., Basit, M., Bradbury, P., Brignac, S., Bumester, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Goev, Gordon, M., Sotway, U., Newton, J., O'Brien, K., Patel, P., Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (17-DEC-1997) Genome Science & Technology Center,
University of Texas Southwester Medical Center, 5323 Harry Hines
Blvd, Dallas, Tx 75235-6959, USA
On Dec 17, 1997 this sequence version replaced gi:2251215.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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100.0%; Pred. No. 2.3;
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/db_xref="taxon:9606"
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100.08; PIC
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HTG: HTGS_PHASE1.
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Continuation (5 of 6) of AC084416 from base 400001 (AC084416 Mus musculus clone rp23-43d
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Evans.G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D.,
Davie,J., Davies,C.J., Davist,C., Fondon,T.,
Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O.,
Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U.,
Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Evans (G.A., Athanasiou, M., Basit, M., Bradbury, P., Brignac, S., Bumesiter, R., Davis, C., English, C., Franklin, T.L., Garner, H.R., Gee, V., Gordon, M., Gotway, G., Grant, O., Hahner, L., Harris, J., Hinson, S., Narayanaswamy, U., Newton, J., O'Brien, K., Patel, P., Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T. and Wilson, F.
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100.0%; Pred. No. 2.2;
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complement(65451.
/rpt_family="Alu"
66069. .66363
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66511. .66757
/rpt_family="Alu"
66827. .67040
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67591. .67869
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67136. .67409
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Ma.J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzeker,M., Miner,G., Mitchell,T., Monabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Petez,L., Pickens,R., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergree,R., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Taber,F., Tamerisa,A., Tansey,J., Taylor,C., Taylor,T., Talsey,J., Taylor,C., Taylor,T., Talsey,J., Taylor,C., Wall,R., Wand,S., Ward-Moore,S., Warren,R., Washington,C.,
Wallington,S., Wald-Moore,S., Warren,R., Washington,C.,
Walliams,G., Wulliams,G., Williamson,A., Wilczyk,R., Wooden,S.,
Weinstock,G., Wulliams,G., Williamson,A., Zorrilla,S., Nelson,D.,
                                                                                                                                                Tamerisa, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length
* (See hitp://www.husc.bcm.lmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 69 contids. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-SRP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 120703 bases at least 040
Consensus quality: 133407 bases at least 030
Consensus quality: 139407 bases at least 030
Estimated insert size: 124919; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CH230-4N16
------ Summary Statistics
Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contins are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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3920: aga of unknown length
10804: contig of 6884 bp in length
10904: gap of unknown length
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contig of 4113 bp in length
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gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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contig of 2945 bp in
gap of unknown leng
contig of 2881 bp in
gap of unknown leng
contig of 2284 bp in
                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
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of 2220 b
unknown 1
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                                                                                                                                                                                                                                                                        (bases 1 to 158769)
                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
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                                                                                                                                                                                                                                           Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                     Worley, K.C.
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                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
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JOURNAL
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This sequence is the entire insert of clone RPI1-125123 The true left end of clone RPI1-89310 is at 99174 in this sequence. The true right end of clone RPI1-400120 is at 40034 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                    1382. 1522

/note="12 repeat: matches 1273. 1423 of consensus"

1585. 1653.

/note="LIMC5 repeat: matches 7729. .7797 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                              /note="5S repeat: matches 1. .42 of consensus" 2846. .2997 /note="MIR repeat: matches 102. .261 of consensus" complement(3929. .4189)
                                                                                                                                                                                                                                                                                    /note="AluX repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="58 copies 2 mer at 73% conserved"
3957, 74181
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/note="match: GSS: Em:AQ012444"
3957, .4156
/note="match: STS: Em:G45158"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3955, .4132)
/note="match: STS: Em:HS351WB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3929, .4189)
/note="match: GSS: Em:AQ577939"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3951. .4071)
/note="match: GSS: Em:AZ485047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3954. .4216)
/note="match: GSS: Em:AQ214300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3960 .4157)
//note="match: 878: Em: 601739"
complement(3962 .4129)
/note="match: GSS: Em: AQ985402"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // note="match: GSS: Em:AZ353055"
Complement(4020, .4152)
                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ346776"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AG019010"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3959. .4102
/note="match: GSS: Em:A2416994"
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/note="match: GSS: Em:AZ369902"
/note=match: 4042, 4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:A2009992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4004. .4203
/note="match: GSS: Em:AQ598220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4020. .4153)
/note="match: GSS: Em:AQ209289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4023. .4178)
/note="match: GSS: Em:AZ306702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ._____(4042, .4166)
/note="match: GSS: Em:AZ020968"
complement(4060, .4203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AZ226345"
4063, .4194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3988, .4199)
/note="match: GSS: Em:AZ030802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:A2116221"
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4082, .4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3962. .4102)
/note="match: STS: Em:M84924"
                                                                                                           /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                      /clone="RPI1-125123"
/clone_lib="RPC1-11.1"
7. 697
                                                                                                                                                         /chromosome~"13"
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                                                                    FEATURES
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the Sanger acc.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromating approached by the Sanger Centre Chromosome 13 Mapoling Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear PRI 04-DEC-2000
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RP11-125123 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human DNA sequence from clone RP11-125123 on chromosome 13.
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of 2489
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/note="Tandem repeat. Forced join. Gap size estimated to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="LiME1 repeat: matches 5679. .5949 of consensus"
16034. .16284
/note="LiME1 repeat: matches 5271. .5590 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /nute="LimB6 repeat: matches 5867. .6172 of consensus"
16849. .17009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Alusg/x repeat: matches 137. .297 of consensus" 17022. .17063
/note-"LIM4 repeat: matches 5807. .5858 of consensus" 17109. .17194. 17198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77888. 19890
/note="L1MB6 repeat: matches 3790. 5813 of consensus"
19891. 20236
/note="L1M4 repeat: matches 2932. 3283 of consensus"
20408. 20571
/note="FRAM repeat: matches 5. 173 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 20. .172 of consensus"
12922. .13067
/note="LiME3 repeat: matches 6001. .6155 of consensus"
13795. .13847
                                                                                                                                                                                                  /note="L1MB3 repeat: matches 5471. .6180 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1M4 repeat: matches 4106. .4184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="LTR16A repeat: matches 359. .423 of consensus"
14465. .14550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /notew"FLAM_C repeat: matches 11. .132 of consensus" 15736. .15983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anotes L2 repeat: matches 2611. .2702 of consensus 14590. .14965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14590. .14965
/note-"L2 repeat: matches 2130. .2516 of consensus"
15236. .15359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16286. 16579
/hote="AluSg repeat: matches 1. .294 of consensus"
16589. 16848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be approximately 225bp by restriction digest data.
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                                                                                                                                                                                                                                                                              /note="AluSq repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote-"MSTD repeat: matches 79. .394 of consensus" 11350. .11501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSc repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                   8187. .8287
/note="MIR repeat: matches 88. .197 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MSTB repeat: matches 1. .426 of consensus"
10159. .10271
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 32. .145 of consensus"
10500. .10613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 21. .134 of consensus"
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17140
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/note="26 copies 2 mer ca 80% conserved"
21041. .21195
                                                                                                         4130. .4203
/note="37 copies 2 mer at 68% conserved"
complement(5247. .5696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:A0582307"
20572. .20646
/note="match: GSS: Em:A2023172"
complement(4082. .4178)
/note="match: GSS: Em:A2110479"
complement(4088. .4203)
/note="match: GSS: Em:B64246"
4130. .4203
                                                                                                                                                             complement(5247. .5696)
/note="match: GSS: Em:AQ127121"
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National John Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrokas, S.L., Ameratunge, H.C., Aero, J.R., Banks, T., Barbaria, J., Banton, J., Binage, K., Blankehburg, K., Bonnin, D., Bouck, J., Bonton, J., Binage, K., Bankehburg, K., Bonnin, D., Bouck, J., Burch, P., Burkett, C., Burrell, K.L., Bytch, N.C., Carron, T.F., Garter, M., Gavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, T., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davia, M.L., Davis, C., Davis, C., Davis, C., Donn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Duyan-Rocha, S., Durbin, K.J., Eerraguto, D., Flagg, N., Ford, J., Escotto, M., Palis, T., Ferraguto, D., Flagg, N., Ford, J., Ester, P., Frantz, P., Gabisi, A., Garo, J., Garcia, A., Garner, T., Garzer, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Harnidoz, J., Hernandez, J., Hernandez, O., Hodgson, A., Hoyues, M., Holloway, C., Harlis, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, S., Katolson, E., Lewis, L.C., Lewis, L., Li, J., Li, J., Li, J., Liu, J., Liu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
21450. .22001
/note="LiMB3 repeat: matches 5635. .6184 of consensus"
22069. .22199
/note="Mix repeat: matches 11. .144 of consensus"
22820. .23059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LiPA5 repeat: matches 5682. .6143 of consensus"
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7.004="Alu30 repeat: matches 18. .311 of consensus"
23876. .43437
                                                                                                                                                                                                                      /note="MIR repeat: matches 5. .262 of consensus"
23173. .23406
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Local Similarity 100.0%; Pred. No. 2.3;
Nes 21; Conservative 0; Mismatches 0; Indels 0;
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Rattus norvegicus
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NOTE: This is a "working draft' sequence. It currently consists of 59 contings. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 141763 bases at least 040 Consensus quality: 149898 bases at least 030 Consensus quality: 157198 bases at least 030 Estimated insert size: 148835; sum-of-contigs estimation Quality coverage: 0x in 020 bases; agarose-fp estimation Quality coverage: 2.1x in 020 bases; sum-of-contigs estimation
                                                                                                                        2 (bases 1 to 169468)
Worley.K.C.
Worley.K.C.
Submitted (20-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064665.
Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
Direct Submission
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.hetp@bcm.tmc.edu
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109272 125082 contig of 15811 bp in length
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137629 144522 contig of 6934 bp in length
144623 150860 contig of 6238 bp in length
15095 155932 contig of 4972 bp in length
15033 160622 contig of 4972 bp in length
160723 160424 contig of 4590 bp in length
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39935 69620: contig of 29686 bp in length
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164248 164347; gap of 100 bp
164348 164467; contig of 3120 bp in length
167468 167567; gap of 100 bp
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14463. .150860
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150961. .155932
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/db_xref="taxon:9606"
/chromosome="18"
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 169,824 genomic DNA of 18q23
Published only in DataBase (2000) In press
C (bases I to 169824)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Dijaylama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Eujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Sujiyama,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP001854 Inear HTG 30-MAY-2000 HOMO sapiens chromosome 18 clone RP11-871M19 map 18q23, WORKING DRAFT SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mall:hattoriègsc.riken.go.jp, Tel:81-42-778-9923, Fax:81-42-778-9924,
                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On May 30, 2000 this sequence version replaced gi:7630226.
....- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
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           163328: contig of 1093 bp in length
163328: gap of unknown length
164797: contig of 1469 bp in length
164687: gap of unknown length
165944: contig of 1017 bp in length
166014: gap of unknown length
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29686 bp i
21056 bp i
18295 bp i
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Homo sapiens DNA, clone:RP11-871M19.
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90776 contig of
109171 contig of
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100.0%; Pre-
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Best Local Similarity
Matches 21; Conserv
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171180 bp DNA linear HTG 04-MAR-2001
Homo sapiens chromosome 15 clone RP11-405A15 map 15, WORKING DRAFT
SEQUENCE, 24 unordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 171180)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                               2.8%; Score 21; DB 2; Length 169824;
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a 35977 c 35308 g 48450 t 1201 others
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Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                100.0%; Pred. M. ...
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Matches 21; Conservative
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Assembly program: Phrap; version 0.960731
Consensus quality: 161737 bases at least Q40
Consensus quality: 16577 bases at least Q30
Consensus quality: 16577 bases at least Q30
Consensus quality: 16577 bases at least Q20
Insert size: 142000; agarose-fp
Insert size: 16880; sum-of-configs
Quality coverage: 6.1 in Q20 bases; agarose-fp
Ouality coverage: 5.1 in Q20 bases; agarose-fp
* NOTE: This is a "working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                             * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30711: gap of 100 bp 35383: contig of 4672 bp in length 35483: gap of 100 bp 40859: contig of 5376 bp in length 40959: gap of 100 bp 85677: contig of 44718 bp in length
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146767: contig of 15306 bp in length
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110625: contig of 11406 bp in length
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163014 171180: contig of 8167 bp in length.
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1603 3185: contig of 1583 bp in length
3186 3285: gap of 100 bp
3286 5525: contig of 2240 bp in length
5526 5625: gap of 100 bp
5626 7859: contig of 2234 bp in length
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contig of 2234 bp in length
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contig of 7331 bp in length
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1502: contig of 658 bp in length
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99220. 110625
/note="assembly_fragment"
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/note="assembly_fragment"
146868. .162913
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23602. .26867
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26968. .30611
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131462. .146767
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                                                             1603. .3185
/note-"assembly_fragment"
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/note="assembly_fragment"
7960. .9703
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15042, .17448
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17549. .20738
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20839. .23501
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40960. .85677
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845. .1502
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AC087675.2 GI:18644833
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Matches 21; Conservative
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M. Unpublished
Barnan, M. Bastlen, W. Budslaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Colangelo, M., Collins, S., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ginde, S., Givelette, M., Graham, L., Grand Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., MacCarthy, M., McEwan, P., McKernan, K., Murphy, T., Mengar, V., Murphy, T., Maylor, J., Nguyen, C., Norman, C. H., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Ribay, R., Rise, C., Rody, P., Schupback, R., Seaman, S., Severy, P., Schaues, S., Stanger Thomann, J., Rosetti, M., Strauss, N., Subramanian, A., Talanas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Yen, N., Volan, S., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammelia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 172628)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-871M19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zembek.L., Zimmer,A. and Zody,M. Direct Submission Submittehed (15-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Feb 11, 2002 this sequence version replaced gi:12229450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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* for the upsp between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* the accession number will be greserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------ Project Information
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/clone_lib="RPCI-11 Human Male BAC"
1 36776 c 36345 g 50098 t 478 others
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109635 122255: contig of 12621 bp in length
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Web site: http://www-seq.wi.mit.edu
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                   HTG 12-JAN-2002
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Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                AC106518 183553 bp DNA linear HTG 12-JAN-
Rattus norvegicus clone CH230-30L6, WORKING DRAFT SEQUENCE, 55
                                                                             0; Gaps
                    Score 21; DB 2; Length 172628; Pred. No. 2.3;
                                                                             0; Indels
                                                                          Mismatches
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                 Db 114256 GGACCTCAGAGTCTCTTCTTG 114276
                                            100.0%; Pr
tive 0;
                                                                                                                                   48 GGACCTCAGAGTCTCTTG 68
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                                                                             21; Conservative
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                           unordered pieces.
                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                             18
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                                                                             Matches
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REFERENCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
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Center: Baylor College of Medicine

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                    Consensus quality: 166054 bases at least Q40
Consensus quality: 171941 bases at least Q30
Consensus quality: 177084 bases at least Q20
Estimated insert size: 167987; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 3.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length
                                                                            Assembly program: Phrap; version 0.990329First call to
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14950: gap of unknown length
21823: contig of 6873 bp in length
21923: gap of unknown length
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        Contact: hgsc-help@bcm.tmc.edu
                                                 Center clone name: CH230-30L6
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HTG 05-DEC-2001
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                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                               AC098697 145 05-DEC-2C Rattus norvegicus clone RP31-387A21 strain Brown Norway, WORKING DRAFT SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (31-OCT-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Dec 5, 2001 this sequence version replaced gi:16554358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 165000; agarose rp Insert size: 185783; sum-of-contigs Quality Coverage: 11.77x in Q20 bases; agarose rp Quality coverage: 10.45x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence, It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 185173 bases at least Q40 Consensus quality: 185494 bases at least Q20 Consensus quality: 185458 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 28242: contig of 28242 bp in length
28342: gap of unknown length
128343 101574: contig of 73232 bp in length
101575 101674: gap of unknown length
101675 185983: contig of 84309 bp in length.
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/clone="RP31-387A21"
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Rattus norvegicus
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Best Local Similarity 100.0

Matches 21; Conservative
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Submitted (12-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Oct 20, 2001 this sequence version replaced gi:16259089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 20-OCT-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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HOMO Sapiens chromosome 2 clone RP11-169L20, WORKING DRAFT
SCOUSNCE, 2 unordered pieces.
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                       Query Match 2.8%; Score 21; DB 2; Length 185983; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 21; Conservative 0; Mismatches 0; Indels 0;
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Sequencing vector: plasmid; 62%
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HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_ACTIVEFIN.
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101675. 185983
1006-*assembly_fragment"
1 38748 c 39092 g 53241 t
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                                         /note="assembly_fragment
clone_end:SP6
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                                                                                vector_side:right"
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/clone_lib="RP31"
1. .28242
                                                                                                      .101574
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Waterston, R.H.
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AC021144 199254 bp DNA linear HTG 07-JUL-2000 HOMO sapiens chromosome 18 clone RP11-451L19, WORKING DRAFT SEQUENCE, 14 unordered pieces.
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Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2008) 1 (2
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On Mar 13, 2000 this sequence version replaced gi:7024036
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Sequencing vector: M13; 84%
Sequencing vector: M13; 84%
Sequencing vector: plasmid; 16%
Chemistry: Dye-primer ET; 84% of reads
Chemistry: Dye-terminator Big Dye; 16% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 195747 bases at least Q30
Consensus quality: 195776 bases at least Q20
Insert size: 202000; agarose-fp
Insert size: 197954; sum-of-contigs
Quality coverage: 5.33 in Q20 bases; sum-of-contigs
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                                1195: contig of 1195 bp in length
1295: gap of unknown length
188741: contig of 187446 bp in length.
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1296. .188741
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clone_end:SP6
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56484 a 35228 c 36736 g 60193 t
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                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606" ,
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone~"RP11-169L20"
                                                                                                                                                                                            Location/Qualifiers
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Waterston, R.H.
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AC021144.3 GI:7232137
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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                contig of 3590 bp in length gap of unknown length length contig of 6290 bp in length contig of 4490 bp in length contig of 4490 bp in length gap of unknown length contig of 5012 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 7624 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length
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contig of 8128 bp in length
contig of 10438 bp in length
contig of 10438 bp in length
gap of unknown length
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contig of 10654 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 9955 bp in length
contig of 9955 bp in length
gap of unknown length
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143960: gap of unknown length
199254: contig of 55294 bp in length.
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/note="assembly_name:Contig15"
102403. .143860
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19783, .29782
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/note-"assembly_name:Contiq5"
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/note∞"assembly_name:Contig8"
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54123 a 44847 c 44725 g 54245 t
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/db_xref="taxon:9606"
/chromosome="18"
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ORIGIN

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Sirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Davar, K., Diaz, J.S., Collymore, A., Carreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Farro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lebozzky, J., Levine, R., Liac, MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McRernan, K., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Rieback, M., Kiley, R., Rise, C., Rogov, P., Rosetti, M., Roy, A., Santos, R., Schueris, S., Schupback, R., Seaman, S., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 18 clone RP11-451L19 map 18, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigillo,J., Vassillev,H., Viel,R., Vo.A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                        Gaps
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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      Length 199254;
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------ Project Information
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-451L19
          DB 2;
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                        100.0%; Pred. ....
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Zembek, L., Zimmer, A. and Zody, M.
          2.8%; Score 21;
00.0%; Pred. No.
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2 (bases 1 to 202032)
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Ouery Match
Best Local Similarity 100.0
Matches 21; Conservative
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MAM 08-APR-1997
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QELVSRDPGHFLILLEQILQKTREVQEKGTYDLLAPLALLFYSTVLCTPHFPPDSDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The G beta gamma sensitivity of a P13K is dependent upon a tightly associated adaptor, p101 cell 89 (1), 105-114 (1997) 97248491
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Location/Qualifiers
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1 (bases 1 to 4692)
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100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-451L19"
/clone_lib="RPCI-11 Human Male BAC"
| 47220 c 44171 g 54695 t 995 others
                                                                                                124779 124878: gap of 100 bp 124879 133231: contig of 8353 bp in length 13322 133331: gap of 100 bp 177276 177375: gap of 100 bp 177376 177375: gap of 100 bp 177376 177375: gap of 100 bp 177376 177375: gap of 15567 bp in length 177376 177375: gap of 15567 bp in length
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68280: contig of 68280 bp in length
                                                          124778: contig of 53038 bp in length
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                    68281 68380: gap of 100 bp
68381 71640: contig of 3260 bp in length
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/product="p101 protein"
/protein_id="CAA71730.1"
/db_xref="GI:1935002"
                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Y10742
Y10742.1 GI:1935001
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/db_xref="taxon:9823"
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KLRT PP PVARCYTYSWNOOSFD I LOE I LLKEQELLQPE I LODEEDEDEEDEEDELDA
GRCAERDSVLSTGSAASHASTLSLASSOASCPTSRQLLTSFVSGLSDGVBSGYNED
I EESAY ERPRERGGHERRGHRRPGGKFNI YKLFKSTSQMVI RRDSRSLEGSPDSGPP
LRRAGSLCSPLOSPTLPPSRAGGSRSLPQPKLSPQLPGMLLAPASRHQRRRPFLSGDE
DPKASTLRYVPGSDR I SKNYDAYSNI RRLENRELLAPASRHQRRRPFLSGDE
                                                                                                                                         TPTSPARRSOPPELPTDAPRHPOPAELGAAPWEESTHOUSHULGMDBWYERNULGM
HLPPEVLCQSLKAEPRPLEGSPAQLFILADMLLYYCRFAARPVLLOYYOTELTFITGE
KTTEIFILASLEGHSAATRAKSGPGSKRIGIDGDREAVPLTLULIYSKGAISGRSR
WSWMEKLCTSVWLSKARCROOFELGSTBALTLUKTEVYKROTPRSKK
                   VTVILLINPVEVQAEFI. DVADKLSTPGPSPHSAY ITLLLHAFQATFGAHCDLSGLHRRL
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G-beta-gamma regulated phosphatidylinositol-3' kinase
Patent: US 5856132-A 1 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                   Score 20; DB 4; Length 4692;
Pred. No. 7.9;
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Stephens,L. and Hawkins,P.Thomas.
G-beta-gamma regulated phosphatidylinositol-3'Kinase
Patent: US 5856133-A 1 05-JAN-1999;
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                                                               Query Match 2.7%; Score 20; DB 6; Length 4692; Best Local Similarity 100.0\%; Pred. No. 7.9; Matches 20; Conservative 0; Mismatches 0; Indels
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Stephens, L. and Hawkins, P.Thomas.
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Lifect Submission (1) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Dec 5, 2001 this sequence version replaced gi:17066657.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempte was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBJ: Sw: SWISSPROY; Tr: TREMBL: Wp: WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone conligs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping the constructed by the Sanger Centre Chromosome 1 Mapping the construction can be found at the constructed by the Sanger Centre Chromosome 1 Mapping the construction can be found at the condition can be found at the constructed by the Sanger Centre Chromosome 1 Mapping the construction can be found at the condition can be found at the constructed by the Sanger Centre Chromosome 1 Mapping the conditions are used to associate primer and the conditions are used to associate primer and the conditions are used to associate
AL607106 36777 bp DNA linear PRI 30-NOV-2001 Human DNA sequence from clone RPII-207N22 on chromosome 1, complete
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RPI1-207N22 is from the library kPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628 CTCCCTGCTGCAGAAGGAGA 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 36777)
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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human.

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL REFERENCE

TITLE

AUTHORS

DEFINITION

ACCESSION VERSION KEYWORDS

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102781 bp DNA linear HTG 24-OCT-2001
Homo sapiens chromosome 8 clone CTD-2168K21 map 8p21, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 102781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 102781)
Polley,A., Wen,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-AUG-1999) Genome Analysis, Institute of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Oct 24, 2001 this sequence version replaced gi:14329018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wen,G., Baumgart,C., Blechschmidt,K., Dette,M., Jahn,N.,
Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A.,
Siddiqui,R., Taudien,S., Schilhabel,M.B., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; 100% of reads
Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.999329
Consensus quality: 97759 bases at least Q40
Consensus quality: 97758 bases at least Q30
Consensus quality: 96720 bases at least Q20
Ouality coverage: 6.97 x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%; Score 20; DB 2; Length 97192;
       gap of 100 bp
16413: contig of 15625 bp in length
                                                                        16414 16513: gap of 100 bp
16514 97192: contig of 80679 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Insitute of Molecular Biotechnoloy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16514. 97192
/note="assembly_fragment"
a 20026 c 20485 g 28511 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CITD Human BAC"
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Center clone name: CTD-2168K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                               /clone="CTD-2168K21"
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                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- Genome Center
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       689 788: gap of
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    789.
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JOURNAL
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                                                                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren B., Linton.L., Nusbaum,C., Lander,E., Ali.A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B., Brown,A. Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangello,M., Collins,S., Collymore,A., Cook,A., Cookel,Y., Colangello,M., Collins,S., Collymore,A., Cook,A., Cookel, DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Fareira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Kalatas,A., Kells,C., Lakocque,K., Jones,C., Kamat,A., Kalatas,A., Kells,C., Lakocque,K., Matthews,C., Macdonald,P., Major,J., Matthews,C., Macdonald,P., Major,J., Matthews,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPherers,R., Mehow,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norman,C.H., O'Connor,T., O'Co
AC107373 97192 bp DNA linear HTG 19-JAN-2002
Homo sapiens chromosome 8 clone CTD-2168K21 map 8, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted 3200 Jah-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 688: contig of 688 bp in Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 14.4 in Q20 bases; agarose-fp Quality coverage: 14.4 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@yenome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 97192)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone CTD-2168K21
                                                                                                                                                                               HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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Web site: http://www-seg.wi.mit.edu
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                                                                        SEQUENCE, 3 ordered pieces.
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                                                                                                                                         AC107373.1 GI:18250049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 97192)
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TITLE JOURNAL

COMMENT

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findPhrapList
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                                                                 Norway rat.
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                                                                                     ORGANISM
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                                         KEYWORDS
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                     VERSION
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                                                                 SOURCE
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Rattus norvegicus clone CH230-8E12, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                              Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                    This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                             This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality 10. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 20; DB 2; Length 102781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 25899 bp in length gap of unknown length contig of 9888 bp in length gap of unknown length contig of 3671 bp in length gap of unknown length
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1455: gap of unknown length
17105: contig of 45650 bp in length
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Best Local Similarity 100.08; Pred. No. 8.7
Matches 20; Conservative 0; Mismatches
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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Balbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Balbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Balbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Balbrooks, S.L., Burbar, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Caracos, S.R., Chacko, J., Chards, D., Chen, G., Chen, C., Chen, C., Chen, C., Chen, C., Chen, C., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, M.L., Dapaer, H., Dougan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragulo, D., Flaggin, D., Ford, J., Ford, J., Ford, J., Ford, J., Hawes, M., Hanilton, K., Hartis, C., Harris, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A., Hernandez, J., Herrandez, O., Hodgson, A., Hoglows, M., Holloway, C., Harrisson, E., Jacobson, B., Jia, Y., Johnson, R., Joliver, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Joliver, S., Lio, W., Louseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martin, C., Liu, J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Mayen, M., Morris, S., Moser, M., Nucken, S., Moser, S., Moser, M., Nucken, S., Marken, S., Marken, S., Marken, S., Marken, S.
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                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Dec 20, 2001 this sequence version replaced gi:15799378.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
               NOTE: Estimated insert size may differ from sequence length
                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
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Human DNA sequence from clone RPI1-72B4 on chromosome 9, complete
                                                                                                                                                        Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 Abases 1 to 134882) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                       Submitted (31-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94989, USA On May 31, 2001 this sequence version replaced gi:7711307. Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
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DOE Joint Genome Institute and Stanford Human Genome Center.
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tive 0; Mismatches 0; Indels 0;
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.8.
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/clone="CTB-147N14"
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http://www.sanger.ac.uk/HGP/Chr9
RP11-7284 is from the library RPCI-11.1 constructed by the group of
pleter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RPI1-72B4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RPI1-72B4 is at 1 in this sequence. The true left end of clone RPI1-18014 is at 142537 in this sequence. The true right end of clone RPI1-36B7 is at 81734 in this
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
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/note="LIMC4 repeat: matches 6822. .7608 of consensus"
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8622. .8704
/note="MBR47 repeat: matches 2242. .2323 of consensus"
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/note="MER47 repeat: matches 2265. 2320 of consensus"
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/note="L1PA3 repeat: matches 5359. .6142 of consensus"
14647. .15016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103413. .1047/3
/note="LIMES repeat: matches 5913. .6162 of consensus"
17298. .17542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1MC4 repeat: matches 7813. .7952 of consensus"
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/note="LiPA3 repeat: matches 4256. .5387 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9785. 9897
/note="L1M4 repeat: matches 5160. 5276 of consensus"
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/note="LlM4 repeat: matches 3504. .3744 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJb repeat: matches 84. .206 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 1852. 2745 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER5A repeat: matches 9. .178 of consensus"
15915. .16173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Alu repeat: matches 233. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 103. .146 of consensus"
5694. .5993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Alusx repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MLT1D repeat: matches 1. .184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MLT1D repeat: matches 1. .417 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="THE1C repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6069. .6317
/note="MIR repeat: matches 15. .262 of consensus"
                                                                                                                                                    Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ib="KPC1-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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1935. .27t
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/note="MIR repeat: matches 15. .262 of consensus"

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32601. 34100

7001. 34100

7001. 34100

7001. 3400

7001. 3590 of consensus.

7001. 3590 of consensus.

7001. 37636

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                                                                                                                                  /note-"AluY repeat: matches 1. .296 of consensus"
18257. .18527
/note-"LLMB3 repeat: matches 5893. .6175 of consensus"
18326. .18645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26961. 27967

/note="LiMB3 repeat: matches 5173. ,6178 of consensus"

27974. 28088

/note="Mass repeat: matches 46. 159 of consensus"

30417. 30572

/note="LiMD repeat: matches 21. 189 of consensus"

30647. 30901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40736. .40792
/note="HAL1 repeat: matches 883. .939 of consensus"
44656. .45707
/note="LiMoz repeat: matches 5193. .6224 of consensus"
50430. .50717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25260. 25323
/note="LIM4 repeat: matches 2510. 2574 of consensus"
25777. 2686 repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg1 repeat: matches 3. .296 of consensus" 21775. .22900
7. /note="LiMed repeat: matches 844. .1489 of consensus" 22902. .23133
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/note="LIM4 repeat: matches 4487. .4585 of consensus" 39151. .39429
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80898. .31021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rnote="LIM4 repeat: matches 2773. .2896 of consensus"
1061. .32002
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Totch="MERLIC repeat: matches 1. .1071 of consensus"
56961. .27967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LiMD repeat: matches 179. .1438 of consensus" 2004. .32557
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40736. .40792
                                                                                                                                                                                                                    /note="L1 repeat: matches 3985, .4104 of consensus" 18647, .18889
                                                                                                                                                                                                                                                                                                                                                                                          //octe="L] repeat: matches 3596. .3984 of consensus"
19316. 19616
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                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 64, .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                    Though Alusa repeat: matches 1. 301 of consensus 19617. .21010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 177. .256 of consensus" 37637. .37941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 1. .304 of consensus"
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17480. .17590
/note="Single clone region. Assembly confirmed by
restriction digest data."
                                                                                     /note="60 copies 2 mer tt 60% conserved"
17915. 18209
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B Birreu, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Baschien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Collinos, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collinos, S., Contropiano, A., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galggan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Illey, I., Johnson, R., Jones, C., Kann, L., Karnen, L., Karlen, J., Larocque, K., Jones, C., Menor, L., Marquis, N., Klehn, J., Larocque, K., Jones, C., Menor, C., Merquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, R., Dieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Mcdurk, J., Mendey, T., Mendey, M., Merand, C., Pilana, C., Pilana, C., Pilana, C., Pilana, C., Riley, R., Spencer, B., Schauer, S., Severy, P., Spencer, B., Trigilio, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vonn, Vonn, Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vonn, C., Submanian, A., Talamas, J., Testaye, S., Leedy, R., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vonn, C., Submitted (01-ApR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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HOMO sapiens chromosome 19 clone RPI1-492P7 map 19, WORKING DRAFT
SEQUENCE, 41 unordered pieces.
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50912. .52140
/note="TIGGER2 repeat: matches 1461. .2718 of consensus"
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 158276)
                                                                                                                    54520. .54839

/note="Alusx repeat: matches 1. .298 of consensus"

56188. .56301

/note="LiM44 repeat: matches 6570. .6692 of consensus"

56527. .56852

/note="LiM46 repeat: matches 4937. .5258 of consensus"

56853. .57142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       od/11. .58606
/hote="liMc4 repeat: matches 7031. .7419 of consensus"
58550. .58886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Limc4 repeat: matches 7261. .7565 of consensus" 58890. .59017
                                                                                                                                                                                                                                                                                                                                                                                                           /note-"L1MB6 repeat: matches 5258. .6004 of consensus"
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                                                           52344. .52629
/note="Alusg repeat: matches 1. .291 of consensus"
54520. .54819
                                                                                                                                                                                                                                                                                                                                         Note="Alusc repeat: matches 1. .290 of consensus" 57143. .57847
                                                                                                                                                                                                                                                                                                                                                                                                                                            57861. 57893
/note="WRR3 repeat: matches 17. .49 of consensus"
58211. .58606
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tive 0; Mismatches 0; Indels 0;
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117213 117312: gap of 100 bp 117313 123367: contig of 6055 bp in length 123468 130252: contig of 6785 bp in length 13053 130352: contig of 6785 bp in length 13053 130352: contig of 8250 bp in length 13053 138602: contig of 8250 bp in length 138603 138702: gap of 100 bp 138703 146693: contig of 8250 bp in length 146694 146793: gap of 100 bp 146693: gap of 146793: gap of 146793: gap of 146793: gap of 167794 158276: contig of 11483 bp in length
     42090; gap of 100 bp
45777; contig of 3687 bp in length
45877; gap of 100 bp
49591; contig of 3714 bp in length
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77729: contig of 4538 bp in length
71829: gap of 100 bp
77477: contig of 5648 bp in length
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63118: contig of 5506 bp in length
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contig of 5770 bp in length
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/note="assembly_fragment"
10904. .12572
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/note="assembly_fragment"
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/chromosome="19"
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                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
On Apr 28, 2000 this sequence version replaced gi:7382520. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                             Assembly program: Phrap, version 0.960731
Consensus quality: 139969 bases at least Q40
Consensus quality: 139969 bases at least Q40
Consensus quality: 151798 bases at least Q30
Insert size: 170000; agarose-fp
Insert size: 154276; sum-of-contigs
Quality coverage: 34 in Q20 bases; sum-of-contigs
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122 221: gap of 100 bp
222 1570: contig of 1349 bp in length
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contig of 1500 bp in length
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23199: contig of 2396 bp in length
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                                                                                                                         Web site: http://www-seq.wi.mit.edu
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gap of unknown length contig of 3176 bp in length gap of unknown length contig of 3500 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACU94124 175335 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-3C23, *** SEQUENCING IN PROGRESS ***,
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
consists of 69 contigs. The true order of the pieces

* is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 141125 bases at least 040 Consensus quality: 14751 bases at least 030 Consensus quality: 152853 bases at least 020 Estimated insert size: 142190; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15633873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329First call to
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Houmania: Eutheria: Primates: Craniata; Vertebrata: Euteleostomi; Bukaryota; Merazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammania: Eutheria: Primates: Catarthini: Hominidae: Homo.

I (bases I to 176601)

Benton. Bankerburge, H.C., Are,J.R., Banks.T., Barbaria,J., Benton. B. Burkerlunge, H.C., Are,J.R., Banks.T., Barbaria,J., Benton. B. Burkerlunge, H.C., Are,J.R., Bonks.T., Barbaria,J., Boute,S., Biteva,M. Bryant. N.P., Buhay.C., Catron. C., Covic. M.C., Cavazos,S.R., Chakofo,J., Chavez,D., Chan,G., Cox.,C., Coyle,M.D., Dathorne,S.R., Davida,M.L., Daya,S.C., Cox.,C., Coyle,M.D., Dathorne,S.R., Davida,M.L., Daya,S.C., Davy,Carrol,J.L., Deform,J.L., Ding,Y., Dinh,H.H., Douthwalte, K.J., Draper,H., Dram,J.L., Ding,Y., Dinh,H.H., Douthwalte, K.J., Draper,H., Dram,J.L., Ding,Y., Dinh,H.H., Douthwalte, K.J., Draper,H., Dugan. Rocha,S., Duthin,K.J., Earlant,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Elago,N., Fordia,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Harrandez,J., Hernandez,J., Hernandez,J., Hernandez,J., Hernandez,J., Hernandez,J., Hernandez,J., Hernandez,J., Howard,S., Hune,J., Jackson,L.E., Jacobson,B., Jaz,V., Johnson,R., Holloway,C., Kraftovic,J., Kelly,S., Khan,U., King,L., Korvah,J., Louis,S., Hume,J., Jackson,L.E., Laody,R., Johnson,R., Holloway,C., Kraftovic,J., Kelly,S., Khan,U., King,L., Korvah,J., Louis,G., Martinez,E., Massey,E., Mawhiney,E., Martinez,E., Massey,E., Mayba,P., Martin,R., Martinez,E., Massey,E., Mayba,P., Martin,R., Martinez,E., Massey,E., Mayba,P., Martin,R., Martinez,E., Wassey,E., Mawhiney,E., Martin,R., Martinez,E., Wassey,E., Mayba,P., Martin,R., Wartin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Many,R., Milla,M., Okuonu,G., Organnse,M., Nolviedo,R., Polcher,R., Sucher,R., Savek,A., Rollada,M., Nolviedo,R., Savek,A., Rollada,M., Nolviedo,R., Savek,A., Tabor,P., Tamerisa,K., Yangan,R., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams,G., Walliams
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AC073581 AC073581 GI:14277165
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Pred. No. 8.9;
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153516: gap of unknown length
154752: contig of 1236 bp in length
154852: gap of unknown length
156912: contig of 2060 bp in length
157012: gap of unknown length
   bp in length
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contig of 1923
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complement(9746. .10048)
/rpt_family="Alusg"
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789. .8075
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206. .8768
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1632. .1681
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1778. .1835
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3076. .8205
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823. .7237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDMA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                  Worley, K.C.
Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                     Department
Worley, K.C.
Direct Submission
Submitted (25-JUN-2000) Human Genome Sequencing Center, Departmen
Submitted (25-JUN-2000) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE LENGIH: This sequence does not necessarily represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
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0.0018261
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Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40 :
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Number of N's in consensus :
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Direct Submission
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Direct Submission

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shaull, S., Rahhal, R., Yao, Z. and Roe, B.A.
Direct Submission
Submitted (05-OCT-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-JAN-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
ON Dec 15, 2001 this sequence version replaced gi:16152276.
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Shaull,S., Rahhal, K., Yao,Z. and Koe,B.A.
Direct Submission
Submitted (15-DEC-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                            AC083892 190390 bp DNA linear ROD 29-JAN-Mus musculus chromosome 1 clone rp23-l16m12, complete sequence.
AC083892
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                                    2.7%; Score 20; DB 9; Length 176601;
100.0%; Pred. No. 8.9;
Live 0; Mismatches 0; Indels 0;
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The University of Oklahoma
Center code: UOKNOR
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tive 0; Mismatches
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complement(10061. .10213)
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/chromosome="1"
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                                                                            Matches 20; Conservative
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                                                       Best Local Similarity
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                       Submitted (29-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries: hunqueryesanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Dec 6, 2001 this sequence version replaced gi:17384553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGA94; version 4.5
Assembly program: XGA94; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 20522 bases at least Q40
Consensus quality: 206730 bases at least Q30
Consensus quality: 206730 bases at least Q30
Insert size: 207564; sum-of-contigs
Ouality coverage: 10.30x in Q20 bases; sum-of-contigs Quality
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                 AL645842.10 GI:17402343
HTG: HTGS_PHASE1; HTGS_DKAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
Web site: http://www.sanger.ac.uk
PROGRESS ***, in unordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.uk
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1. .208964
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 204877 bases at least Q40 Consensus quality: 208297 bases at least Q40 Consensus quality: 208297 bases at least Q30 Consensus quality: 208090 bases at least Q20 Insert size: 205000; agarose-fp Contigs Quality coverage: 5.9 in Q20 bases; agarose-fp Quality coverage: 5.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13, M78615; 100% of reads Sequencing vector: M13, M78615; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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156041 210995: contig of 54955 bp in length.
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2079 4482: contig of 2404 bp in length
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1. .1978
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                                                                 Center code: WIBR
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Stren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boqualavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gart, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Prizer, R., Poliza, V., V., Lander, A., and Zody, M., Rheeler, J., Wu, X., Prizer, S., Prizer
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Homo sapiens clone RP11-16P4, WORKING DRAFT SEQUENCE, 10 unordered
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Submitted (21-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 1, 2000 this sequence version replaced 91:6453955.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 210995)
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100.0%; Pred. No. 8.9;
Live 0; Mismatches 0; Indels 0;
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fragment_chain:3"
147358. .149656
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Best Local Similarity
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REFERENCE
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Query Match
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Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (29-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CBIO 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Citone requests: clonerequest@sanger.ac.uk
On Jan 19, 2002 this sequence version replaced gi:18181773.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4: version 4.5
Assembly program: XGAP4: version 4.5
Chemistry: Dye-terminator Big Dye: 100% of reads
Consensus quality: 215543 bases at least Q40
Consensus quality: 215698 bases at least Q30
Consensus quality: 215698 bases at least Q20
Insert size: 215938; sum-of-routigs
Insert size: 198378; 6.5% error; adarose-1p
Quality coverage: 13.45x in Q20 bases; sum-of-contigs Quality
coverage: 14.75x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                 AL662927
216038 bp DNA linear HTG 30-JA Homo sapiens chromosome 1 clone RP11-16P4, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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                                                                                                                                                                                                                   .,0
                                                                                                                                                                     Length 210995;
                                                                       900 others
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209672 216038: contig of 6367 bp in length.
Location/Qualifiers
                                                                                                                                                                  Score 20; DB 2;
Pred. No. 8.9;
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Center code: SC
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/note="assembly_fragment"
156041. 210995
/note="assembly_fragment"
57929 a 47946 c 47269 g 56951 t
                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL662927.8 GI:18250578
HTG; HTGS_PHASE1; HTGS_CANCELLED.
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/db_xref="taxon:9606"
                                                                                                                                                                2.7%; Score 20;
100.0%; Pred. No.
tive 0; Mismatc
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/clone_lib="RPCI-11.1"
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Best Local Similarity
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AC073693 230372 bp DNA linear HTG 29-JUN-2000 Mus musculus clone RP23-152L22, WORKING DRAFT SEQUENCE, 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Consensus quality: 223517 bases at least Q30
Consensus quality: 223517 bases at least Q30
Consensus quality: 224719 bases at least Q30
Estimated insert size: 228000, agarose-fp estimation
Estimated insert size: 228572; sum-of-contigs estimation
Quality coverage: 7.65 in Q20 bases; agarose-fp estimation

Quality coverage: 8.64 in Q20 bases; sum-of-contigs estimation

NOTE: This is a working draft sequence. It currently

* consists of 19 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                2.7%; Score 20; DB 2; Length 216038;
100.0%; Pred. No. 9;
                                                                                                                                                         101 others
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                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                       vector_side.left"
209672. 216038
a 50140 c 47530 g 56342 t 1
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Center Code: JGI
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DOE Joint Genome Institute.
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100.0%; Pre-
                         vector_side:left
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                                                                                                                                                                                                                                                                                                                                                                       628 CTCCCTGCTGCAGAAGGAGA 647
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clone_end:SP6
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                                          clone_end:T7
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4258:
6473:
6573:
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unordered pieces.
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Matches 20; Conserv
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1188
2716
2816
4159
4259
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Consensus quality: 184430 bases at least Q40
Consensus quality: 20805 bases at least Q30
Consensus quality: 20805 bases at least Q30
Consensus quality: 214713 bases at least Q20
Estimated insert size: 203000, agarose-fp estimation
Estimated insert size: 203000, agarose-fp estimation
Quality coverage: 9.19 in Q20 bases; agarose-fp estimation
Quality coverage: 9.19 in Q20 bases; sum-of-contigs estimation
NOTE: This is a "working draft" sequence. It currently
consists of 57 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Mus musculus clone RP23-167E16, WORKING DRAFT SEQUENCE, 57
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Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Seconder Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 240842)
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/clone_lib="RPCI mouse BAC library 23"
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132683: gap of unknown length
149580: contig of 16897 bp in length
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of 1649 bp in length
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ORIGIN
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Length 240842;

DB 2; 9;

Score 20; Pred. No.

2.7%; 8

Query Match Best Local Similarity

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FRCOFLNKNYFV!VNADILITOVWKSTVLLPQTPNWATTLTDMQ1TER1FYKETFFSLN
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LODVDPQTHQVYFKSSCPPLEMDLIDEKMFCNCSEKLGLRVTNLPRGTAIVGSEPLI
TLVKILINRMVKNNT-HLCPTLILEPTLILESGLLILEFTIRERKCVRI."
179 c 168 9 220 L
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Liess, B., Appel, M.J. and Osterhaus, A.D.
Characterization of phocid herpesvirus-1 and -2 as putative alpha-
                                                                                                                                                                                                 UL52' helicase-primase complex homolog [phocid herpesvirus type-2 PhHV-2, host*Phoca vitulina, isolate 7848, Genomic, 788 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                              and gammaherpesviruses of North American and European pinnipeds
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GenBank Staff at the National Library of Medicine created this
entry (NCBI gibbsq 176141) from the original journal article.
This sequence comes from Fig. 4a.
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Neisseria gonorrhoeae.
Neisseria gonorrhoeae
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
Neisseria.
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/note="This sequence comes from Fig. 4a"
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                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
1 (bases 1 to 788)
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/protein_id="AAB35973.1"
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Pred. No.

100.0%;

Best Local Similarity

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VFGGSWGSTLSLAYAQTHPERVKGLVLRGIFLCRPSFTAWLNEAGGVSRIYPEQWQKF
VAPIAENRRNRLIEAYHGLLFHQDEEVCLSAAKAWADWESYLIRFEPEGVDEDAYASL
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                     Molecular cloning and characterization of a proline iminopeptidase
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Submitted (02-AUG-1993) NAN H ALBERTSON, GENERAL AND MARINE
MICROBIOLOGY, DNIVERSITY OF, GOTEBORG, CARL SKOTTSBERGS GATA 22,
GOTEBORG, 413 19, SWEDEN
1. 2582
11. 2582
                                                                                                          (bases 1 to 82)
Bhat,K.S., Gibbs,C.P., Barrera,O., Morrison,S.G., Jahnig,F.,
Stern,A., Kupsch,E.M., Meyer,T.F. and Swanson,J.
The opacity proteins of Neisseria gonorrhoeae strain MS11 are
encoded by a faill complete genes
Mol. Microbiol. 5 (8), 1889-1901 (1991)
                                                                                                                                                                                                                                                                                                             To (bases 1 to 82)
Bhat.K.S., Gibbs,C.P., Barrera,O., Morrison,S.G., Jahnig,F.,
Stern,A., Kupsch,E.M., Meyer,T.F. and Swanson,J.
The opacity proteins of Neisseria gonorrhoeae strain MS11 are
encoded by a family of 11 complete genes
Mol. Microbiol. 6 (8), 1073-1076 (1992)
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/note="upstream activation site typical for -24 -12
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Apr;6(8):1073-6]]
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/db_xref="SPTREMBL:051058"
/translation="MNPARKKPSLLFSSLLFRSAGGK"
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1448. 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="roline iminopeptidase Pip"
/protein_id="CAA80948.1"
/db_xref="GI:396840"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from MS11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Neisseria gonorrhoeae"
/strain="MSO1-1X, derived from MS
                                           gene from Neisseria gonorrhoeae
Mol. Microbiol. 9 (6), 1203-1211 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SWISS-PROT:P42786"
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/note="-24 -12 promoter"
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Albertson, N.H. and Koomey, M.
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Albertson, N.H.
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501. .1433
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DB 1; Length 2582;

2.5%; Score 19;

Query Match

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baf gene; lipopolysaccharide biosynthesis; terminal inverted repeat; waaA gene; waaC gene; wlbA gene; wlbB gene; wlbC gene; wlbD gene; wlbE gene; wlbE gene; wlbE gene; wlbL gene; wlbT gen
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                                                                                                                                                                                                                                                 2957 bp DNA linear PAT 31-JAN-2002 Compositions and methods for the prevention and diagnosis of human gnonskan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2957)
Fikrig, E., Barthold, S.W., Ijdo, J. and Sun, W.
Compositions and methods for the prevention and diagnosis of human granulocytic ehrlichiosis
Patent: JP 2001502528-A 6 27-FEB-2001;
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1 (bases I to 15389)
Allen, and Maskell,D.
The identification, cloning and mutagenesis of a genetic locus
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gene, waaA, waaB & wlbA,B,C,D,E,F,G,H,I,J & L genes.
      Gaps
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506 c 829 g
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30-SEP-1997 JP 1998516827
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Topology: Linear;
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JP 2001502528-A/6.
                                                                                                    1141 GCATCTTCATCCACTCCT 1123
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JP 2001502528-A/6
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                                                                   663 GCATCTTCATCCACTCCCT 681
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Bordetella pertussis
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PERQLEVCHRWAGATGRPVIALNSTREGEDAMETEA IGALQAHKAATPKPLILLIJPRH
PQKFDEAAAQLQAAGLAYARKSAGSGEPGPHIDVLLGDTLGEMPFYYAAADVAIVGGS
FARLGGONLIEBCAAGATPVIVGPHTFNFKDAARDAIAGAALRAPDARTALDWALQLL
AEPARRQAMSEAARAWTAAHAGATRYTLDALEDWLG"
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WLVRQTRGVRHGLDWRSAREPLVSLEYNVRHRVEFWQPAVVRQRKLAALTFGYNYAGS
PDFGLQAFGRAAQADDAPADPGRRMLHLAADRGYAVIMPSASRDDKLWPEDDWRAVFR
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IGKGQLQQAWLPYDFPGATRRFLARHAPRGGLLMEREVWPNLJAAARAGGVPMALVSA
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GLTHLSAALGRPT1G1YRASTPVRTPLVGPSYTASLGDRGASPSREAVLASVEQALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MGRGVYTLALRGLAPLIWLWMWRRARRAGGGWELFAPARFCRAG
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                                                                                                                                                                                                               Submitted (10-AUG-1995) D.J. Maskell, Imperial College of Science, Technology, and Medicine, Dept of Biochemistry, Exhibition Road, London SW7 Ayv, UK

3 (bases 1 to 15389)
                                                                                                                                                                                                                                                                                                                      Reeves, P.R., Hobbs, M., Valvano, M.A., Skurnik, M., Whitfield, C., Coplin, D., Kido, N., Klena, J., Maskell, D., Raetz, C.R.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Trends Microbiol. 49, 495-503 (1996)
Polysaccharide genes have been named in accordance with the
Bacterial Polysaccharide Gene Nomenclature scheme.
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required for lipopolysaccharide biosynthesis in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial polysaccharide synthesis and gene nomenclature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="FGATPQPTYLDSPVLDGLAALAAQGAPTA" complement(289. .1575)
                                                      Molecular microbiology. 19 (1), 37-52 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bordetella pertussis"
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/gene="waaC"
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/gene="waaC"
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/transl_table=11
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                                                                                                                                                                                           Direct Submission
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                               pertussis
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FWTRPOEYYDAARWRGKWEWDGGAFNNQASHYVDLLDWLVQFVBSVYAYTATLARRIE
AEDTGVAALBRRHGARGSINVTMLTYPQNLESSITILGERGTYRVGGVAVAYTDEWRY
AEPHPDDDKIREANYETTSVYGFGHPLYYDNVINCLRGDCEPETDGREGLQSLALLTA
IYRSARDGVRIPLPLD"
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VEPDTCNIKVSEIEAKITPRTKAIIPVSLYGQCGDMDEVNAVAARHGLPVIEDAAQSF
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DRDSVWAQFTVWVPNREAVIAQLKEAGIPTAVHYPRPIHAQPAYEOYAEGAGATPVSD
DLAARVMSLPMHPDLDEATQDKIVAALRQALN"
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LAGALAAVKLHIPVAHVEAGLRSFNLRMPEEVNRILTDRISRMLFTPTDSATRHLAAE
GOSGEKVVQVGDVMYDVALHHGARVTAEGRALAAHGLRPGGYVLATIHRAENTDDAQR
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YAALIATDSGGVQKEAFFHRIPCVTLRDETEWTELVDAGWNRLAPPVSSAVVAQAVQD
                                                                                                                                                                                                                                                                                                                      NPEALQAAEAATGARPESSLSDMLAQGNADALVLATPSGLHPWQATEVAQAGRHVVSE
KPMATRWEDGKRMVKACDEAGVRLEVVKQNRRNATLQLVKKATEQGRFGRTYMVTVNV
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19:37-52(1996)"
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AL670463 30425 bp DNA linear PRI 07-FEB-2002 Human DNA sequence from clone RPl3-145E22 on chromosome X, complete sequence.
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Cambridgeshire, GB10 15A, UK. E-mail enquirics.
Our heb B, 2002 this sequence version replaced gi:18477112.
During sequence assembly date is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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AHCGLSVPAEDPAALAAALHGLRTLPAAERQAMGRRGKDYVLARHDYPVLAQOFLDAV
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DLPLTLPPGPGRTPGVERVAHRDDDEHSWHLYAIRJHPQAPLKCDDFJVRMTENGJGC
SVHYVPLHLQPYWRDRYGLTPDMYPHSQAAFEGMASLPIYSRMTDADVQRVIASVRQL
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LPCALPYMRERGLDPRRYAHVPNGVPVTEYSSPDFDNPDYLRVRAQ1RQLREGCDFVL
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IDPATLCISPAAIERAITPRTRAIVPVHYGGLSCDMDSILEIARKHGLKYIEDAAHAL
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9074. 9667
/yote="wibG"
/note="gene referred to as bplG in Mol. Microbiol.
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                             /codon_start~]
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7890. .9077
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Matches 19;
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw:, database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          нэвээн/
Human DNA sequence from clone SC22CB-33B7 on chromosome 22 Contains
GSS2, complete sequence.
                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/HGP/ChrX
RP13-145E22 is from the library RPCI-13.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryola, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was generated from part of bacterial clone contigs \limsup the Cancesome 22, constructed by the Sanger Centre Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib*"RPCI-13.1"
5744 c 5296 g 91
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/clone="RP13-145E22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Further information
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Matches 19; Conserv
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http://www.sanger.ac.uk/HGP/Chr22
During sequence assembly data is compared from overlapping clones.

Murer differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone SC22CB-33B7 The true left end of clone RP1-222E13 is at 25472 in this sequence. The true right end of clone RP2-919B11 is at 27970 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="clone RP1-222El3; aaaaaca in this entry; insertion"
/replace="aa"
1594. .1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="clone RP1-222E13; gcc in this entry; substitution"
/replace="gtc"
967. .969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1365. 1367
/note="clone RP1-222E13; ggc in this entry; substitution"
                                                                                                                                                                                                                                                   Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL, WP., WORMPEP: Information on the WORMPEP database can be found at the WORMPEP cac.uk/Projects/Celegans/wormpep SC2CB-33B7 is from the human chromosome 22-specific cosmid library (SC2CB) constructed at the Sanger Centre by Mark Ross and Cordelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802. .804
/note="clone RP1-222E13; ggg in this entry; substitution"
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/note="clone RPI-222E13; gtt in this entry; substitution"
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/note="clone RP1-222E13; tga in this entry; substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="clone RP1-222E13; tag in this entry; substitution"
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/note="clone RPI-222E13; tt in this entry; deletion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alu repeat: matches 234. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ... ... v. comsensus"
Anote-"Alusc repeat: matches 1. .309 of consensus"
1365. .1367
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/note="AluSx repeat: matches 2. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Alu repeat: matches 68. .109 of consensus"
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//note="MIR repeat: matches 33. .167 of consensus"
2617. .2637
Mapping Group. Further information can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="22"
/clone_lib="SC22cB"
/clone="SC22CB-33B7"
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626. .628
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985. .1056
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2055. .2057
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659. .806
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1772, .2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'replace="gac"
507. .1513
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2980. .2982
/note-"clone RP1-222E13; cgt in this entry: substitution"
/replace-"cat"
                                                                                                                                                                       3136. .3138
/note="clone RP1-222E13; cgc in this entry; substitution"
/replace="ctc"
                                                                                                                                                                                                                                              7016 "L2 repeat: matches 2699. .2748 of consensus" 3602. .3614 /note="clone RP1-222E13; cga in this entry; substitution" /replace="caa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /replace="gtg"
4470. .4472
/note="clone RP1-222E13; ttg in this entry; substitution"
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5899. 5901
/note="clone RP5-919B11; cgg in this entry; substitution"
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/note="clone RP1-222E13; tct in this entry; substitution"
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/note="clone RP1-222E13; gcc in this entry; substitution"
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/replace="tt"
5598. .5600
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740ce-"Aluxx repeat: matches 121. .299 of consensus"
7418. .5420
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/note="clone RPI-222E13; ag in this entry; deletion"
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/note="clone RP1-222E13; tg in this entry; deletion"
/note="MIR repeat: matches 245. .262 of consensus"
                  2638. .2946
/note="Alusg repeat: matches l. .307 of consensus"
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/note="AluSx repeat: matches 1. .311 of consensus"
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/note="AluJb repeat: matches 5. .311 of consensus"
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6327. .6636
/note="AluSx repeat: matches 1. .312 of consensus"
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/note="AluSx repeat: matches 1. .121 of consensus"
                                                             2947. .3127
/note="MIR repeat: matches 34. .245 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5603. 5903
/note="AluY repeat: matches 1. .301 of consensus"
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3867. .3869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear PLN 11-JAN-2001
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                 /note="Alusg repeat: matches 1. .301 of consensus" 6970. .6972 /note="clone RP1-222E13; aaa in this entry; substitution"
                                                                                                                                                 /note="clone RP1-222E13; att in this entry; substitution"
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                                                                                                                                                                                                                                                                                                                                          /note="FLAM_C repeat: matches 122. .142 of consensus"
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/note="LTR26 repeat: matches 512. .579 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MLT1F repeat: matches 234. .354 of consensus"
                                                                                                                                                                                                                           /note="MLT1H repeat: matches 460, .526 of consensus"
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7482. 7616 repeat: matches 1. .311 of consensus"
7483. .7616
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note="match: GSS: Em:AQ214568 Em:AQ214591"
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Best Local Similarity 100.0%; Pred. No. 33;
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SVSTISTESAYTSSSVSDIAASTLEVGTSEATVSFSTDIPATPSTLSSPASSS
SYSTISTESAYTSSSVDIAASTLEVGTSEATVSFSTDIPATPSTLSSPASSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MCNRQPKAVDLPPNYSCPHLLSFQSVEFNTNPTACDDVFCKRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EISASNGYEKKLDSSIGNPGEKAVSPVHIEDFQSPQIYKFKNLSLRDEMVSDCVFADE
VPLASLFVENVCNETIPSQSCVRLKINDKTRKVDASALEKKSCLLPNSSGTLTDQRGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISLISMISPRPNLSTHHFNLGFQPLSQQTSFSGSSTQNPHSSSTCKKAFCFQCISESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEKKYNDFLESLFKKYGRDTSDIADEVDLATGEIIVNNGHLEALKTKDDIWDPTFNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical serine/threonine repeat containing protein; agglutin-like" /protein; agglutin-like" /protein_id="CAC21474.1" /db_xref="G1:2188965"
any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="nominal overlap with p11E10 S. pombe chromosome 1"
                             number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following splice donor/acceptor sites. CDS are numbered using the following cosmid name). 01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                       sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. BAC pBHA10 is overlapped at the 5' end by pl pliE10, EMBL entry SPAP11E10, accession number ALS1493, and at the 3' end by cosmid cl40, EMBL entry SPAC140, accession number ALB163191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENOA_CHICK, alpha enolase, (433 aa), fasta scores: opt: 141, E():0.18, (27.9% identity in 201 aa)"
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/protein_id="CAC21475.1"
/db_xref="G1:12188966"
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/gene="SPAPBIA10.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1. .1672)
/gene="SPAPBIA10.01c"
/note="SPAP11E10.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1, .1672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="BAC pBlA10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain-"972h-
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/product.efgeranylgeranyl transferase type i"
/product.efgeranylgeranyl transferase type i"
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MAYFRAIMAKKEYSLRALUTGFLIMNPAHYTWAYRFQILNHTPSYIONELEWLDE
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YSQENKLTNEULERDIYNNSAWNHRFYVLFFTSKWYSWSLEEELNYLKDKTLFAPDNO
SAWNYLCGWLDMSGESKLDNLIANLRRNLFALHKPLLEFLAMYEPSSSEEIYQKLANE
                                                                                                                                                                                                                                                     VTEFTSMIVNLPYSKTKVEDFDSQQVMGNDMNIIIVVSGTIRFDGKKPHVFSYRSATT
QPDDTIFKDPVMDEQVQKLEEKMSSLVVNDPELAQKVGRLRQFFEKYGLEAGSKPSPL
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                                                                                                                                                                                                                          /translation="MESSVKYAQEFVQRYYSSLDTNRNGIAEFYRENSLILWNGKPMQ
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/gene="SPARBIA10.05"
/note="PAPBIA10.05, len:286, SIMILARITY:Caenorhabditis
elegans., O76471, cytoplasmic signalling transducer, (554
aa), fasta scores: opt: 133, E():0.75, (23.9% identity in
                          Q9NPJ8, p15-2a protein, (142 aa), fasta scores: opt: 214,
E():8e-07, (28.0% identity in 118 aa)"
/codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Match to PF01239 PPTA, Protein prenyltransferase alpha subunit repeat Score 46.95" complement(6663. .6755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /yeur....r...
Journal of the PF01239 PPTA, Protein prenyltransferase alpha subunit repeat Score 47.18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /hote="Match to PF01239 PPTA, Protein prenyltransferase
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/note="SPAPB1A10.03, len:201, SIMILARITY:Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="transtitttacag, splice branch and acceptor" complement(6457, .6462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ctaacaattaaag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="gtcagt, splice donor sequence" complement(join(6204 . 6411,6463 . 7139)) /gene="cwpl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(6204. .6411,6463. .7139))
                                                                                                                                      /product="putative nuclear export factor"
/protein_id="CAC21476.1"
                                                                                                                                                                                                                                                                                                                                                                                           /note="gtatgt, splice donor sequence"
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                                                                                                                                                                                            /db_xref="GI:12188967"
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                                                                                                                                                                                                                                                                                                                                        4913, .4918
/qene="SPAPBIA10.03"
                                                                                                                                                                                                                                                                                                                                                                                                                         4952. .4964
/gene="SPAPB1A10.03"
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/gene="SPAPB1A10.03"
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                                                                                                              /label-SPAPB1A10.03
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EIARKRVSLESDHPDKSGQVIDLATGQILDKQTEDIDDDRNKSAVSKSLVRHPHRLKM
                                                                                                                                                                                                 LPFGIQSAHPYISSLNSNYPTTWHFASHYYPTDSKQLVKYHPTEVHPSWTVEEPVHYN
TYDGVVNEPNSSVIIEELDDDYDELNDPMNNNDTPITNSTHSAQMSNLPTHDSMDIDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MGRLRKRFNEKGROSGIQKMLNLKRARLHRSVREQESSSEVHAN
PEPDNQDSNAEILIDVPKEERQKRKQELKDQLLKENEGSISSKKKKRLDKYIENKLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetyltransferase; baf; Bvg accessory factor; degT-type regulatory protein; formyltransferase; GlcNAc transferase; glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amidotransferase, heptosyltransferase; lipopolysaccharide blosynthesis; nucleotide sugar epimerase/dehydratase; oxidoreductase; transferase; ovidoreductase; transferase; upp-N-acetylquocosamine 2-epimerase; waaA; waaB; wlbA; wlbB; wlbC; wlbB; wlbE; wlbB; wlbB; wlbH; wlbJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clinical Veterinary Medicine, University Of Cambridge, Madingley Road, Cambridge, Cambridgeshire, CB3 0ES, UK
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(URL; http://www.sanger.ac.uk/Projects/B_pertussis/) CDS are
numbered using the following system eg BbLFS1.01c. Bb (B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putalive ATP dependent RNA helicase"
/protein_id="CAC21479.1"
/db_xref="G1:12188970"
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                                                                                                                                                                                                                                                                                                           /gene="SPAPBIAI0.06c"
complement(join(9783. .13046,13094. .13381))
/gene="SPAPBIAI0.06c"
/note="SPAPBIAI0.06c, len:1184"
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                                                                                                                                                                                                                                                                                      complement(join(9783. .13046,13094. .13381))
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/label=SPAPB1A10.06c
/label=SPAPB1A10.05
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Bordetella bronchiseptica
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/gene="BbLPS1.03"
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                                                                                                                                             Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons supplemented by a specially developed Hidden Markow Model. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg. 949 or ttg) which is preceded by an upstream ribosome binding site sequence (optimally $-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
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ADLCVVACWYHMLPSRLRDLFRLGAVGLHASRLPELRGGAPLNWATLAGFERTAVTLF
ALGDGVDDGPVYGQEAIDVGPNDYTGELVARCNAASVVLVERCISGII.NGSLVPAVQD
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AAVYGAPGQILCLPGGQVVVATGKGAIE1EEAEDJGGQSVMVALRRSSHRRFRSQS"
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WWVDEPMSPRDRIARCAEGRAAATMKKYDEDLACFGRDNIGKST"
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                           (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
bronchiseptica), LPS1 (cosmid name), .01 (first CDS), c
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/protein_id="CAA07641.1"
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/note="BbLPS1.02, unknown, len: 262 aa"
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/organism="Bordetella bronchiseptica"
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/dh_xref="GI:3451484"
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/clone="cosmid BbLPS1"
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/transl_table=11
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dehydrogenase (formyltransferases domain) (902 aa), fasta scores; Opt: 199 z -score; 243.2 E(): 2.7e-06, 27.1% identity in 225 aa overlap, and to e.g. TR:050378 (EMBE:U10425) ferric exochelin biosynthesis gene fxbA from Aryobacterium smegmaris (360 aa), fasta scores; opt: 395 z-score: 264.3 E(): 1.8e-07, 29.4% identity in 286 aa overlap. Also similar to the Crterminus of a hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //note-*BbLps1.05, probable formyl transferase, len: 274 as some sinilarity to many Met-tRnA formyltransferases, e.g. FMT_BACSU methionyl-RNA formyltransferases, fasta scores; opt: 266 z-score: 333.9 E(): 2.4e-11, 26.0% of methionyl and some overlap. Also similar to the C-terminus of a hypothetical protein within Salmonella typhimurium putative 4 aminoarabinose lipid A modification operon PR:05225 (EMBL:AF03667) or 713 (660 aa), fasta scores; opt: 337 z-score: 411.2 E(): 1.2e-15, 30.4% identity in 207 aa overlap. Contains Pfam match to entry PF00551
                                                                                                                                                                                                                                                                                                                                                                                                           AGVPATWFATHQTALLERIERHPGFELGIHPNRNNLLSAGSAQSAEGVLDAALALAPG
CRSVRSHSLTQSTRLLALFADRGLGHECNALIPWDAGIPLRPWRHWDGTTVRVPHCWE
DDIACLAGWPLEGDAFYWYDPDGLNVLDFHPIHVYLNTETLERYEASRPVHRDSAALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mkFvAlgrhEILLRTIEMLV7AGHELAGVLTAAPAPEYRADVDD
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HGGDLPRYRGNACQAWALIQGEPAIGLCVHYMVADELDSGDVIAKAMLDVDHHTTIGT
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DVVKHINASGHPYAGAFFYFESNAYRVDEAOWIDGGAYLAVPGQVAGRNPDGSVDVAC
                                                                                                                                                                                                                                                                                                                                                                                /translation~"MKFARISDIDPGSPETWRGKVFLSFDIDWAEDFVLLDTLELIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00551 formyl_transf, Formyl transferase, score 68.90, E-value 1.1e-18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="BbLPS1.04, probable formyl transferase, len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein within Salmonella typhimurium putative.
4-aminoarabinose lipid A modification operon TR:052325 (EMBE.AF036677) orf3 (660 aa), fasta scores; opt: 395 z-score: 264.3 E(): 1.18-07, 29.4% identity in 286 aa overlap. Contains Pfam match to entry PF00551 formyl_transf, Formyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="possible RBS upstream of BbLPS1.04"
                                                                                                                                                                                          /product="hypothetical protein BbLPS1.03"
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/db_xref="G1:3451486"
1609. .2328
/gene="BbLPSI.03"
/note="BbLPSI.03, unknown, len: 239 aa"
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/protein_id="CAA07643.1"
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/transl_table=11
/product="putative formyl transferase"
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LLEARLEMET HPM TREDECTOR TO THE TREATMENT OF THE TREATMEN
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QGRKSKNGISNELQHYSQWTNYFLRVLTVIYSKPINIYVTAMBDTHELNLETGQILTQ
YVPQIRASVLNQILGLTDVVGRIVVNAKTGARGLILEGSEGTYAKNRLDNRTACKIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKNLFKWILSKDEKEQKPVWTPYEVNERKYEERHKREQLLMK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQYNISTTWGEAMIQDEFRKIQQSVI"
complement(2082. .2486)
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/product="ORF6"
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/transl_table=11
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                  /product="ORF2"
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ADTWYLSKRLAGATGRLIENWAALIHDAETCYTLHYLDDGLDTGDIVAGEIGISD
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3541...3798
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GMLSVHKTWDYKNNTGFMPTKTKSSIREIPLDDEFINFIDQLPPTDDGRLLPSLSNNA
VNKTLRKIVGREVRVHSLEHTYASYLIAHDIDLISVSQVLGHENLNITLEVYAHQLQE
QKSRNDEKIKQMMTKGQNALKPHG"
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MELKLQDNVNVDEDITLYDYFKQWCGVYKKPTVSKITYKAYINSQRKIELFFGDKKLK
SITATEYQRVLNSYAKTHAQDTVERFNVHVKACIEMAVHEGYIKRNFCKFAKINAKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptocuccus thermophilus temperate bacteriophage 01205, complete
                                                                                                                                                                                                                                                                                                                                                     /note*"Pfam match to entry PF00551 formyl_transf, Formyl transferase, score 82.00, E-value 1.9e-22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus thermophilus temperate bacteriophage 01205.
Streptococcus thermophilus temperate bacteriophage 01205
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence analysis and characterization of phi 01205, a temperate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-FEB-1997) Department of Microbiology, University
College, Cork, College Road, Cork, Ireland
Location/Zualifiers
1. 43075
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nley.E., Fitzgerald,G.F., Le Marrec,C., Fayard,B. and van
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Stanley,E., Fitzgerald,G.F., Le Marrec,C., Fayard,B. and van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteriophage infecting Streptococcus thermophilus CNR21205
Microbiology 143 (Pt 11), 3417-3429 (1997)
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bacteriophage 01205"
/strain-"CNR21205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; Score 19; DB 1; Length 41642;
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/protein_id="CAA07644.1"
/db_xref="G1:3451488"
/db_xref="SPTREMBL:087978"
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/note="putative integrase"
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/product="ORF1"
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Andersea I to 58747)

R Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Capapolano, A., Chang, J., Chazaro, B., Brown, A., Camarata, J., Camarata, J., Camarata, J., Camarata, J., Canarato, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Galagan, J., Garad-Pierre, N., Ferreira, P., FitzHugh, W., Galagan, J., Garad-Pierre, N., Hagos, B., Heaflord, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kalias, A., Kells, C., LaRocque, K., Liu, G., MacLen, A., Kells, C., Landers, T., Lehoczky, J., Levine, R., Mathews, C., Macdonald, P., Marot, J., Marquis, N., Mathews, C., Macdonald, P., Marot, J., Marquis, N., Mathews, C., Macdonald, P., McRernon, K., McPheeters, R., Mellin, J., Nowib, C., Norman, C.H., Phunkhan, K., Miley, R., Schuers, S., Severti, M., Roya, A., Santos, R., Schauer, S., Schupback, R., Stanco, R., Schauer, S., Severti, M., Roya, A., Santos, R., Schauer, S., Severti, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Londer, M., Lavis, N., Zambek, L., Zimmer, A. and Zody, M., Direct Submission, L., Zimmer, A. and Zody, M., Direct Submission, L., Zimmer, A. and Zody, M., Submission, L., Zimmer, A. and Zody, M., Submission, L., Submission, L., Zimmer, A. and Zody, M., Submission, L., Zim
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SSKLGISTNKLNRILTLEQLPDEELLARMGELCK"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-472123
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1DEAHHYKAKTYLKITEYYSNSIVLMFTGTPARLDGSGFDDIADDIVLGKSVKWLQDN
0N APFKYYSPSLIDTTNLKKRGGEFTKKSVDDTMKRVIYGDVIRHYEKLAKGKQAIV
YTHSVEASSYSWTFNEGGTYSIAISKTPPEVRDAMQAFRGKLITMVNCELFTBG
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KKDPHPISONIGMEGVDIKAHVNNYILVPPSNNSKGYYEWDTVHSPKOGSIITEAPL
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LLLRCVDPEITYHLAKMANNTQEPLGDKEFERTFKSMLDKEIRRIGIDND"
7360. 8874
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KEENPOKKEPRALPELAVAKGLNKTHVITLENGKVAIYDPERGYYQKDYRYAYQLIY
VLEPTENETKCRNVLEPLISNMSREYERNNYMDFEPEYRDYRRFILVNNGIYDKRKK
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FLAQNLPVGWIKDRQKPLDFFNPTKDKPVYWHDFNFNWDENEAKKAAVVVWVTQ"
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                                                      /evidence=not_experimental/product="ORF10"
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/note="putative primase"
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/product="ORF15"
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/product="ORF16"
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contig of 716 bp in length
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28235: contig of 691 bp in length
                                                                                                                              p of 100 bp contig of 704 bp in length p of 100 bp contig of 690 bp in length
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f 702 bp in length
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31539: gap of 100 bp
32234: contig of 695 bp in length
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3851: contig of 712 bp in length
51: gap of 100 bp
34669: contig of 718 bp in length
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45918: contig of 694 bp in length
46018: gap of 100 bp
46716: contig of 698 bp in length
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37912: contig of 708 bp in length
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38815 39508: contig of 694 bp in length
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4103: contig of 700 bp in length
41203: gap of 100 bp
41914: contig of 711 bp in length
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45250: contig of 708 bp in length
43620: gap of 100 bp
44316: contig of 696 bp in length
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contig of 710 bp in length
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55559: contig of 696 bp in length
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33851: con+
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41103: cont
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29039: cont
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38714: cont
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43520: con
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contigs. Kuns of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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76 23408: contig of /1...

79 23508: gap of 100 bp

79 24199: contig of 691 bp in length

70 24199: contig of 691 bp in length

70 7ap of 696 bp in length
                                                                                                                                                                                                             1979: contig of 698 bp in length 1679: gap of 100 bp
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4017: contig of 710 bp in length
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f 709 bp in length
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80: contig of 694 bp in length
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14569: contig of 776 bp in length
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19394: contig of 716 bp in length
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Numnucry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

no bec 8, 2001 this sequence version replaced gi:15020939.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with rhis sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following absembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found a
                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                      AL392047 59314 bp DNA linear PRI 07-DEC-2001 Human DNA sequence from clone RPI1-189M6 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-189M8 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP5-933E2 is at 57315 in this sequence. The true right end of clone RP11-675023 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chrl0
RP11-189M8 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
                                                                                                               Gaps
                                                                                                            0
                                                 Length 58747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Further information can be found at
                                                                                                            0; Indels
                                                    DB 2;
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18957 a 10703 c 11134 g 18520 t
  100 bp
                                                                                                            Mismatches
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                                                                                    Pred. No.
                                                    .5%; Score 19;
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/chromosome~"10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-189M8"
                                                    2.5v,
100.0%; Pre-
55560 55659: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL392047.11 GT:17426975
                                                                                                                                                                                                 129 GACTIGAGACAGTIGACAA 147
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                                                                                                            19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
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Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Birren, B., Linton, L., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chargero, B., Choepel, Y., Colangelo, M., Caulymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., McGwan, P., McFernan, K., Meldrim, J., Manthews, C., Micol, R., Norbu, C., Norman, C., W., Warphy, T., Naylor, J., Muyop, T., Noure, C., Norl, D., Oliver, J., Retta, R., Riebeack, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Schamon, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Travis, N., Travis, N., Travers, N., Travers, N., Travers, N., Viel, N., Ye, W.J., Ye, W.J., Young, G., Land, J., Zanne, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                               ACLO7830 62832 bp DNA linear HTG 24-JAN-2002 Mus musculus clone RP23-230L20, LCW-PASS SEQUENCE SAMPLING. ACL07830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-JAN-2002) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 62832)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-230L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This record contains 78 individual
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100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Center
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                                                                                                                                                                           Db 41192 ACACAGCCAAATCATCAAC 41174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC107830.1 GI:18308533
HTG; HTGS_PHASE0.
                                                                                                                               565 ACACAGCCAAATCATCAAC 583
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5468 5567: gap of 100 bp 5568 6272: contig of 705 bp in length 6273 6372: gap of 100 bp 7072: contig of 700 bp in length 7073 7172: gap of 100 bp 7073 7912: contig of 740 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13599 13698: gap of 100 up
13699 14393: contig of 695 bp in length
14394 14493: gap of 100 bp
14494 15131: contig of 638 bp in length
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28190 28876: contig of 687 bp in length
28877 28976: gap of 100 bp
28977 29681: contig of 705 bp in length
               gap of 100 bp 1488: contig of 709 bp in length gap of 100 bp 2258: contig of 670 bp in length gap of 100 bp 100 bp 3078: contig of 720 bp in length
                                                                                                                                                                                                                                                                                                                                                                                              8012: gap of 100 bp 8733: contig of 721 bp in length 8833: gap of 100 bp 9557: contig of 724 bp in length 9657: gap of 100 bp 10374: contig of 717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15132 15231: gap of 100 bp
15232 15894: contig of 663 bp in length
15895 15994: gap of 100 bp
15995 16697: contig of 703 bp in length
16698 16797: gap of 100 bp
17494: contig of 697 bp in length
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2896 13598: contig of 703 bp in length
3599 13698: gap of 100 bp
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19930: contig of 703 bp in length
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202799: contig of 719 bp in length
20849: qap of 100 bp
21567: contig of 718 bp in length
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23190: contig of 723 bp in length
23290: gap of 100 bp
24004: contig of 714 bp in length
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                                                                                                                                             3079 3178: gap of 100 bp 3179 3850: contig of 672 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04: gap of 100 bp
24834: contig of 730 bp in length
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28089: contig of 699 bp in length
contig of 679 bp in length
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22367: ~~
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27290: cont
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2359 3078: col
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29 50828: gap of 100 bp 103 bp in length 29 51531: contig of 703 bp in length 12 52323: contig of 692 bp in length 13 53423: gap of 100 bp 100 bp 15 53344: gap of 100 bp 15 53344: gap of 100 bp 100 bp 15 53343: contig of 688 bp in length 15 53343: contig of 688 bp in length
29682 29781: gap of 100 bp
29782 30478: contig of 697 bp in length
30479 30578: gap of 100 bp
30579 31264: contig of 686 bp in length
31265 31364: gap of 100 bp
31365 32071: contig of 707 bp in length
                                                                                                                                    32978: gap of 100 bp
33695: contig of 717 bp in length
3395: gap of 100 bp
34515: contig of 720 bp in length
34615: gap of 100 bp
35324: contig of 709 bp in length
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36153: contig of 729 bp in length
36253: gap of 100 bp
36978: contig of 725 bp in length
37078: gap of 100 bp
37778: contig of 700 bp in length
                                                                                                     32072 32171: gap of 100 bp
32172 32878: contig of 707 bp in length
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48320 contig of 706 bp in length
48321 48420: gap of 100 bp
48421 49135: contig of 715 bp in length
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50728: contig of 712 bp in length
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2: gap of
54743: ~.
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48320: cont
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Gaps 0 DB 2; Length 62832; 33; 0; Indels 2.5%; Score 19; DB 100.0%; Pred. No. 33; stive 0; Mismatches Query Match
Best Local Similarity 100.0
Matches 19; Conservative

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<sup>144</sup> ACAATACTCTTAAAGGCAT 162 ò

<sup>53511</sup> ACAATACTCTTAAAGGCAT 53493 Dp

Page 49

RESULT

SOURCE

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100 bp
of 702 bp in length
100 bp
of 693 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp
f 715 bp in length
100 bp
f 731 bp in length
                                                                100 bp .
of 690 bp in length
                                                                                                100 bp
f 710 bp in length
                                                                                                                                                                                                   100 bp
f 740 bp in length
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21000: gap of 100 bp
21734: contig of 734 bp in length
                                                                                                                                                                   100 bp
of 728 bp in length
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                                                              HTG 03-FEB-2002
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
                                                  AC109187 73648 bp DNA linear HTG 03
Mus musculus clone RP24-329N2, LOW-PASS SEQUENCE SAMPLING.
AC109187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                Nusbaum, C. and Lander, E.
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                          1 (bases 1 to 73648)
Birren, B., Linton, L., Nusbaum, C
Mus musculus, clone KP24-329N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone name: 329_N_2
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                                                                                                           GI:18482108
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Submitted (16-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jan 19, 2002 this sequence version replaced giil6973071.

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with this sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least as compressions and repeats; all regions were covered by the teat assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: PRBL; SW:, current prepares.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISSEROT: Tr., TREMEL. WP., WORNEEP; Information on the WORNEEP database can be found at the fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPI-141A19 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP1-141A19 is at 1 in this sequence. The true left end of clone RP5-885E17 is at 93761 in this sequence. Location/Qualifiers
                                                                                                                                              Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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vecToR: pBAce3.6
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contig of 721 bp in length
p of 100 bp
                                                                                35; gap of 100 bp 34649; contig of 714 bp in length 49; gap of 100 bp 35487; contig of 738 bp in length
                                                                                                                                                                                                                                                                                                                                                                             25; gap of 100 bp
3857; contig of 732 bp in length
57; gap of 100 bp
39577: contig of 720 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of 100 bp 56: contig of 689 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154: gap of 100 bp 46032: contig of 678 bp in length
33090: contig of 726 bp in length
                              90: gap of 100 bp
33835: contig of 645 bp in length
                                                                                                                                                                                                   87: gap of 100 bp
36324: contig of 737 bp in length
                                                                                                                                                                                                                                                              4: gap of 100 bp
7108: contig of 684 bp in length
                                                                                                                                                                                                                                                                                                                     p of 100 bp contig of 717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66: gap of 100 bp
41158: contig of 692 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51581: contig of 643 bp in length
81: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 718 bp in length
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contig of 739 bp in length
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HTG 04-JUL-2001
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/note="Sequence from overlapping clone RP11-450E3
(AL606474) Assembly confirmed by restriction digest."
18799 c 17532 g 28857 t
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Best Local Similarity 100.(
Matches 19; Conservative
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AL590432 95760 bp DNA linear PRI 16-JAN-2002 Human DNA sequence from clone RPl1-141A19 on chromosome 1, complete

95760 bp

sednence.

DEFINITION AL590432/c RESULT 56

Db 56958 CAGGAAGCTGAGAATTGC 56940 236 CAGGAAGCTGAGAAATTGC 254

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.85187

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/clone="CITD-2058112"
/clone_lib-"CIT Approved Human Genomic Sperm Library D"
On Aug 16, 2001 this sequence version replaced gi:8096474.
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complement(7389. .7827)
/rpt_family="LIME"
/evidence-not_experimental
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/db_xref="taxon:9606"
/chromosome="6"
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    COMMENT
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The incleotide sequence of this BAC clone was generated by Combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Butheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases I to 106763)
Shimizu.N. and Asakawa, S.
Direct Submission
Submitted (22-MAY-2000) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shimanomachi, Shinjuku-ku, Tokyo Tel:81-3-3351-2370, Fax:81-3-3351-2370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear PRI 30-0CT-2001
                                                                                    Oryza sativa
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
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                                                                                                                                                                                  Sasaki,T., Matsumolo,Ť. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1163_G04
                                                                                                                           Spermatophyta; Magnoliophyta; Liliopsida; Poáles; Poaceae;
Ehrhartoidoae; Oryzeae; Oryza.
1 (bases 1 to 106253)
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* the accession number will be preserved.
Location/Qualifiers
                                                      Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1163_G04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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/db_xref~"taxon:4530"
/chromoscwe="7"
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Homo sapiens
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AP003815
AP003815.1 GI:14595155
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(TC)n" _experimenta (TA)n"	not_ 830_ y="M	175 Y~"AT_rich" not_experiment	908 Y="A1 not_e 577	Y = 2	not_experimenta 605 y="CT-rich"	not_experimenta (1560915872) y="L2"	not_experimen 537 y="MiR"	not_experimenta 847 y="AluSx"	not_experimenta 126 y="AT_rich"	not_experimenta 416 y≈"AluYb8"	not_experiment 506 y="AT_rich"	not_experimenta 875 y="Lipai6"	not_exper 236 y="Alusx" not exper	267 Y-"(GGGA)n" not experiment	603 y="L1PA16"	394 Y="LTR1"	725 y="L1PA16	992 y="(TA)n" not experiment	311 y="(TA)n" not experimen	(2231322608) y="Alusx"	not_experimenta 098 Y="(T)n"	/evidence=not_experimental complement(23395, .23693)
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/rpt\_family\*"Alusg"

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S Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bebrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnih, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnih, D., Bouck, J., Bouck, S., Blateva, M., Brown, M., Bryant, N.P., Buhay, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Cleveland, C.D., Cox, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Dany, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, R.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gao, J., Garcia, A., Garner, T.,
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Rattus norvegicus clone CH230-6B13, *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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100.0%; Pred. No. 34;
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complement(25985. 26220)
/rpt_family="Mily"
/evidence=not_experimental
27269. 27291
/rpt_family="AT_rich"
/evidence=not_experimental
complement(28687. 29229)
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/evidence=not_experimental
30984. 31037
/rpt_family="(TA)n"
/evidence=not_experimental
31115. 31235
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/evidence=not_experimental
25106. .25411
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 69 contings. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15624692.

Center: Baylor College of Medicine
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Consensus quality: 10312 bases at least 030
Consensus quality: 110661 bases at least 020
Estimated insert size: 90316; sum-of-contigs estimation
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Assembly program: Phrap; version 0.990329First call to
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Submitted (03-A0G-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 129641)
DOE Joint Genome Institute and Stanford Human Genome Center,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 5 clone CTC-534A2, complete sequence.
AC008560
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DOE Joint Genome Institute and Stanford Human Genome Center.
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105661: gap of unknown length
107264: contig of 1303 bp in length
107364: gap of unknown length
               bp in length
                                                                                                     in length
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gap of unknown length
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contig of 1318 b
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                            gap of unknown 1 contig of unknown 1 contig of 1372 b gap of unknown 1 contig of 1120 b gap of unknown 1
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contig of 1559 b
gap of unknown l
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contig of 1176 b
gap of unknown l
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DOE Joint Genome Institute.
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PRI 03-OCT-2001
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Doc Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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1 (bases 1 to 120856)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTD-2318A17, complete sequence.
AC016620
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100.0%; Pred. No. 34;
Live 0; Mismatches 0; Indels 0;
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >-40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
www-shgc.stanford.edu
Quality: Phrap Quality >>40 99.5% of Sequence:
Estimated Total Number of Errors is 0.7.
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/db_xref="taxon:9606"
/chromosome="5"
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DOE Joint Genome Institute.
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HTG 05-OCT-2001
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Submitted (19-07-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                        Gaps
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On Sep 23, 2001 this sequence version replaced gi:8699977.
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Length 129856;
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Best Local Similarity 100.6
Matches 19; Conservative
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                              Assembly program: Phrap; version 0.990329
Consensus quality: 114463 bases at least 040
Consensus quality: 126469 bases at least 020
Consensus quality: 136159 bases at least 020
Estimated insert size: 138198; sum-of-contigs estimation
Cuality coverage: 2.8x in 020 bases; agarose-fp estimation
Quality coverage: 2.8x in 020 bases; sum-of-contigs estimation
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16224: gap of unknown length
25186: contig of 8962 bp in length
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contig of 9176 bp in length
gap of unknown length
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Web Site: http://www.hgsc.bcm.tmc.edu/
Notact: hgsc-help@bcm.tmc.edu
Contact: Project Information
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Center: Baylor College of Medicine
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                                                                        Center project name: HMOP
Center clone name: RP11-91K9
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unknown length

2.5%; Score 19; DB 2; Length 139629;

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Query Match
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Tel.81-298-38-7441, Fax:81-298-38-7468)
The nuclectide sequence of this BAC clone was generated by combining Monsanto and KGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Caps between the contigs are represented as runs of N. The order of the gaps between the correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP003809 139629 bp DNA linear HTG 04-JUI Oryza sativa chromosome 7 clone 0J1116_D12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:0J1116_D12
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                                                                                                                                                                                                                                                                                                                               Score 19; DB 2; Length 138725;
Pred. No. 34;
                                                                                                                                                                                                                                               26855 g 40143 t 2436 others
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133622: contig of 3393 bp in length
133722: gap of unknown length
136582: contig of 2860 bp in length
136682: gap of unknown length
138725: contig of 2043 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="0J1116_D12"
40427 a 29835 c 29223 g 39787 t
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                                                                                                                                                        /organism*"Homo sapiens"
/db_xref*"taxon:9606"
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/db_xref="taxon:4530"
/chromosome="7"
                                                                                                              Location/Qualifiers
1. .138725
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                                                                                                                                                                                                     /chromosome~"3"
/clone="RP11-91K9"
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Best Local Similarity 100.0%; Pr
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Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakikinias.afirc.go.jp, URL:http://rgp.dna.affrc.go.jp/, TFD:81-298-38-741, Fax:81-298-38-7468)

NOTE: It currently consists of contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Homo sapiens chromosome 18 clone RP11-26813 map 18, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 142388)
                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (14-NOV-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                            APUU4335 UNA 11near HTG 15-N OVYZA SALIVA CHROMOSOME 7 CLONE P0483G08, *** SEQUENCING IN APOGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
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Oryza sativa
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                                                            0; Indels
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Query Match
Best Local Similarity 100.0%; Pred. No. 24,
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/db_xref="taxon:4530"
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                                                                                                                                                    Db 48406 GCAACTGGCCAAGCAGAAG 48424
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                                                                                                                    214 GCAACTGGCCAAGCAGAAG 232
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HTG 30-NOV-2001
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 142603)
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142603 bp DNA linear HTG 30-NOV Canis familiaris clone RP81-234H11, WORKING DRAFT SEQUENCE, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 19; DB 2; Length 142388;
100.0%; Pred. No. 34;
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                             57781 57880: gap of 100 bp
57881 70671: contig of 12791 bp in length
                                                                               70672 70771: gap of 100 bp 70772 95778: contig of 25007 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
          57780: contig of 11794 bp in length
                                                                                                                                                                                                                                                                                                                                                            /clone_lib∸"RPCI-11 Human Male BAC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"assembly_fragment"
15183. 20848
/note-"assembly_fragment"
20949. 27902
/note-"assembly_fragment"
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 1174. .2606
/note="assembly_fragment"
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5016. .6468
/note="assembly_fragment
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                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
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                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /clone="RP11-26813"
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70772. .95778
                                                                                            /chromosome~"18"
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Spaces Ito 142388)

Baldwin, J., Barran, N., Backerly, R., Boqualavkiy, L., Boukhgalter, B.,
Baldwin, J., Sarran, N., Beckerly, R., Boqualavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreitz, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grah, C., Kann, L., Karatas, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, R., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, R., McLaughlin, J., Meldrim, J.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Plasfaye, S., Tifrell, A., Vasallev, H., Vo, A., Wheeler, J., Wu, X.,
Prizert, C., Mark, A., and Zody, M., Wheeler, J., Wu, X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01.007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Strect, Cambridge, MA 02141, USA on May 25, 2000 this sequence version replaced gi:7133525. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Assembly; program: Phrap; version 0.960731 Consensus quality: 13379 bases at least Q40 consensus quality: 137445 bases at least Q30 consensus quality: 139434 bases at least Q20 lnsert size: 137000; agarose-fp react size: 141088; sum-of-contigs Quality coverage: 4.8 in Q20 bases; sum-of-contigs Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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45886: contig of 9564 bp in length
45986: gap of 100 bp
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-26813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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1174 2606: contig of
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5016 6468: contig of
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27902: cont
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36222: cont
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                                                  Unpublished
  AUTHORS
                                                    JOURNAL
                                                                               REFERENCE
                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haphighi, P., Ho, S.-E., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-G., Legaspi, R., Maduro, C.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Land Green, E.D.
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (30-NOV-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid: n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrao; version 0.990319 Consensus quality: 1415% bases at least 040 Consensus quality: 1417% bases at least 020 Insert size: 91000; agarose-fp Insert size: 142303; sum-of-contigs Quality coverage: 8.69x in 020 bases; sum-of-contigs Quality coverage: 8.69x in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8113: contig of 8113 bp in length 8213: app of unknown length 35526: contig of 27313 bp in length 35626: gap of unknown length 78460: contig of 42854 bp in length 78560: app of unknown length 142603: contig of 64027 bp in length.
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                                                                                                                                                                                                                                                 NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
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35627. 78480
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JOURNAL
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JOURNAL
     AUTHORS
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ACU16611 145899 bp DNA linear HTG 18-JUL-2000 HOMO sapiens chromosome 5 clone CTD-2197B7, WORKING DRAFT SEQUENCE,
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Submitted (04-DE7-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:7710184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 134277 bases at least 040
Consensus quality: 142520 bases at least 030
Consensus quality: 143768 bases at least 020
Estimated insert size: 145000; pulse field gel estimation
Estimated insert size: 145449; sum-of-contigs estimation
Quality coverage: 5.12 in Q20 bases; pulse field gel estimation
Quality coverage: 5.11 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft' sequence. It currently
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that lave
* provided by the submittor.
* This sequence as soon as it is available and
* the accession number will be preserved.
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* The accession number will be in length
* This accession of the accession
                                                                                                      Gaps
                                                                                             0;
            2.5%; Score 19; DB 2; Length 142603;
100.0%; Pred. No. 34;
                                                                                             0; Indels
Query Match
Best Local Similarity 100.08; Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
                                                                                                                                                                                                                     Db 105204 CTCCCTGCTGCAGAGGAG 105222
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                                                                                                                                                                              628 CTCCCTGCTGCAGAAGGAG 646
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ES I (Dasses I to 151548)

Burdy, D.M. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrocks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Brieva, M., Brown, E., Bromin, D., Bouck, J., Bowie, S., Brieva, M. Brown, E., Brown, M., Bryant, N.P., Bulay, C., Bourell, K.L., Byrd, N.C., Carron, T.F., Carter, P., Cavazos, S.R., Chacko, J., Chenge, C., Chen, C., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.D., Davy, Carroll, L., Ding, Y., Dinh, H., Douthwaite, K.J., Draper, H., Dugan, Poolan, R., Doughne, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Georaguto, D., Flagg, N., Footer, T., Gaster, P., Harnis, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hame, J., Jackson, L.E., Jacobson, B., Johnson, R., Liu, J., Liu, T., Liu, M., Liu, M., Liu, M., Martinez, E., Massey, E., Master, M., Mall, R., Martinez, E., Massey, E., Master, M., Mall, R., Martinez, E., Massey, E., Moser, M., Nayledo, R., Packen, M., Mauzer, M., Mall, R., Packen, M., Martinez, E., Massey, E., Master, R., Packen, M., Martinez, E., Massey, E., Warth, R., Packen, M., Parter, M., Parter, M., Naylen, N., Nayledo, R., Packen, M., Packer, M., Mauser, M., Nayledo, R., Packen, M., Packer, M., Mauser, M., Nayledo, R., Packen, M., Packer, M., Martinez, E., Massey, E., Warth, R., Packen, M., Packer, M., Maylen, R., Naylen, R., Naylen, R., Sacher, S., Tamerisa, R., Tamerisa, R., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfred, S., Tanger, M., Tang, B., Tang, M., Tanger, M., Tanger, M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC106459

151548 bp DNA linear HTG 12-JAN-2C
Rattus norvegicus clone CH230-207G10, *** SEQUENCING IN PROGRESS
***, 63 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 2; Length 145899;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                            /clone_lib-"CalTech human BAC library D" / 27496 c 26688 g 44356 t 1005 others
124854: contig of 2284 bp in length
124954: gap of unknown length
132024: contig of 6970 bp in length
132024: gap of unknown length
145899: contig of 13875 bp in length.
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                                                                                                                                                                                                                                            /organism~"Homo sapiens"
/db_xref~"taxon:9606"
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%; Sco
Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
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                                 124955
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132025
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AC106459
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Consensus quality: 130235 bases at least Q40
Consensus quality: 138462 bases at least Q30
Consensus quality: 143966 bases at least Q30
Estimated insert size: 134069; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 2.7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 63 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                  Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length contig of 3369 bp in length gap of unknown length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                             Center project name: GKYJ
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unknown length

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of 3538 bp in length
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gap of unknown 1
contig of 2734 by
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contig of 2943 b
gap of unknown l
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Sirren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bodelson, S., Bodelson, M., Bodelson, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lohson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Marduis, R., Medulim, J., McDewar, P., McGurk, A., McKernan, K., McPheerers, R., Marquis, N., McEwan, P., McGurk, J., Norman, C.H., O'Connor, T., O'Donnell, P., Ollvar, T.M., Peterson, K., Flere, N., Fisani, C., Pollara, V., Raymond, C., Killey, R., Stohman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., dastilev, H., Viel, R., Wo, A., Wu, X., Wyman, D., Ye, W. J., Lander, A. and Zody, M. Lehec, Cambridge, MA 02141, USA

Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Stren, B., Linton, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Cooke, P., Dakrallano, K., Dewar, K., Dasses I to 154984)

Barna, N., Bastlen, Y., Boguslawkiy, L., Boukhgalter, B., Brown, A., Camarata, J.S., Codge, S., Goyette, M., Graham, L., Hagos, B., Heaford, A., Cocke, P., Dastellano, K., Dawar, K., Diaz, J.S., Dodge, S., Ferreira, P., Patzugh, M., Graham, L., Hagos, B., Heaford, A., Lakocque, K., Liu, G., MacLenn, R., Johnson, R., Johnson, R., Johnson, R., McKernan, K., McDwan, P., McMan, P., McGwan, P., 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                     Score 19; DB 2; Length 151548;
gap of unknown length
contig of 1387 bp in length
app of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 1539 bp in length
contig of 1539 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-2K18
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                                                        Submitted (OlymAr-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 1, 2001 this sequence version replaced gi:11415189.

All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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* runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
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                                                                                                                                  114: gap of 100 bp 2762: contig of 1648 bp in length 862: gap of 100 bp 100 bp 2868: contig of 6 bp in length 968: gap of 100 bp 100 bp 1825: contig of 3757 bp in length 11792: contig of 4967 bp in length
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38759 56570: contig of 17812 bp in length
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1 38034 c 38648 g 38686
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                                                                                                                                                                                                                                                                                                                                           ACO16390 156784 bp DNA linear HTG 08-NOV-2000 HOMO sapiens clone RP11-30J7, WORKING DRAFT SEQUENCE, 13 unordered pieces.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156784)
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                Gaps
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                                                     DB 9; Length 154984; 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-30J7
Unpublished
                                                                                                             0; Mismatches
                                                                                     Pred. No.
                                                        2.5%; Score 19;
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     /rpt_family="MLTlF1"
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ACO16390.4 GI:9966971
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                                                                                                             Conservative
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                                                                                  Local Similarity
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COMMENT

Gaps

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1209 others

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                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JAN-2001) Masahira Hattori, The Institute of Physical Band Chemical Research (RKEN), Genomic Sciences Center (GSC); and Chemical Research (RKEN), Genomic Sciences Center (GSC); 1-7-22 Sueliro-chou, Tsurumi-ku, Vokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Dec 19, 2001 this sequence version replaced gi:12275508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC022644 160355 bp DNA linear HTG 01-MAR-2000 Homo sapiens clone RP11-28A20, WORKING DRAFT SEQUENCE, 32 unordered
                                                   PRI 20-DEC-2001
                                                                                 Homo sapiens genomic DNA, chromosome 11q clone: RP11-30J7, complete
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 157959)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 19; DB 9; Length 157959; 100.0%; Pred. No. 35; 0; Indels 0
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-28A20
                                                         DNA
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                                                                                                                                                                                                                          Homo sapiens DNA, clone:RP11-30J7.
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                                                   157959 bp
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                                                                                                                                                                   AP003101.2 GI:17939959
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AC022644.2 GJ:7139692
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                                                                                                                                                                                                                                                        sapiens
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RESULT 71
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Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M.
                                                                                                                                                                                    Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 1, 2000 this sequence version replaced gi:6910664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 141286 bases at least 040 consensus quality: 151099 bases at least 030 consensus quality: 151099 bases at least 030 consensus quality: 154621 bases at least 020 lineset size: 176000; agarose-fp insert size: 157255; sum-of-configs Quality coverage: 3.1 in 020 bases; agarose-fp Quality coverage: 3.4 in 020 bases; sum-of-configs
                                                                                                                                                                                                                                                                                                                                        Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
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of 1195 bp in length
100 bp
of 1752 bp in length
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of 1601 bp in length
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contig of 1367 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93: gap of 100 bp 33031: contig of 2938 bp in length
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contig of 2293 bp in length
                                                                                                                                                                                                                                                                                                            repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
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18337: ~
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26976; _
76
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15417: cont
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35424: cont
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35525 38714: cont
38715 38814: gap of
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4078 5829: cor
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102827 103926: gap of 100 bp 102927 111471: contig of 8545 bp in length 111472 111571: gap of 100 bp 111572 136106: contig of 2455 bp in length 1156107 136206: gap of 100 bp 100 bp 136207 160355: contig of 24149 bp in length.
                                                               48: gap of 100 bp 51862: contig of 4214 bp in length 62: qap of 100 bp
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                           33: gap of 100 bp 47548: contig of 4815 bp in length 48: gap of 100 bp
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82627 89240: contlg of 6614 bp in length
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38815 42633: contig of 3819 bp in length
42634 42733: qap of
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51963 57095: contig of 5133 bp in length
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60996: contig of 3801 bp in length
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HS919B11 160725 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome 22 clone RP5-919B11 map q12.3-13.32, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160725)
Griffiths, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Structure, Hinxton, Cambridgeshire, Submils (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CD10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:6981834.
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Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C. and
                                       Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haugen, E.
       AUTHORS
                                                                                                                     JOURNAL
                                                                                                                                                        REFERENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160903)
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AC092812.2 GI:16874869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Quality coverage: 10.27x in Q20 bases; sum-of-contigs Quality
                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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94742 .131462
/note="assembly_fragment:03896"
                                           coverage: 9.26x in Q20 bases; agarose-fp
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/note="assembly_fragment:02994"
66947. .94641
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/note="assembly_fragment:05273"
42852 c 42211 g 37262 t
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/note="assembly_fragment:02354"
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/db_xref="taxon:9606"
/db_ctrfomcome="2"
/map="q12.3-13.32"
/clone="RP5-919B11"
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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality) - 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                         Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J., Ivey, R.G. and
                                                                                                                                                                                                                                               Submitted (28-JUL-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 160903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-NOV-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Nov 9, 2001 this sequence version replaced gi:15027765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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                                                                                                                                                                                                                                                                                                                                                                    Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Pirrap; version 0.990319
Consensus quality: 160823 bases at least 040
Consensus quality: 160829 bases at least 030
Consensus quality: 160891 bases at least 030
Consensus quality: 160803 bases at least 020
Insert size: 15125; 11.5% error; agarose-fp
Coulity coverage: 9.2x in 020 bases; sum-of-contigs
Quality coverage: 8.7x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: plasmid; 46% of reads
Sequencing vector: plasmid; L08752; 54% of reads
Chemistry: Dye-terminator ET; 89% of reads
Chemistry: Dye-terminator Big Dye; 11% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: University of Washington Genome Center
Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: RPII-536F12 (sc0172)
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3': RP4-798D13 (UWGC:sc0214) AL354679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: chr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- Genome Center
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                                                                                  (bases 1 to 160903)
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Direct Submission
Unpublished
                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                 Haugen, E.D.
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607 <800 1187 1159 5855 5938	<800 3376 3399 2293 231	<800 462 <800 2570	1543 22 <800 419	8146 2145 2089 5175 5		9442 9507 3159 3166 981 970	1008 994 1340 1322 5441 5404	898 891 838 827 633 <800	705 <800 121 <800 6404 6434	2255 1619 1599	1356 792 <800 2701	9507 383 <800 1235	1062 461 <800 515	12275 2113 2089 7676	8146 8	3 3162	1812 1813 1470 1481	2020 2089			4622 4577	5%; Score 19; DB 9; Length 160903; .0%; Pred. No. 35;	datches 19; conservative 0;	415 CATCATTGGCCAGATTATC	Db 96922 CATCATTGGCCAGATTATC 96904	RESULT 75	AL157702	N Human DNA sequence from clone RPII-18B16 novel pseudogene, complete sequence.	ACCESSION ALIS7702 VERSION ALIS7702.10 GI:10086046	i	OKGANISM Homo sapiens Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;		TITLE Direct Submission	Cambridgeshire, CBIO ISA, UK. E-mail enquiries:	COMMENT On Sep 11, 2000 this sequence version replaced gi:10039651.
Bglii 		6080 5938	2067 2062	5523 5938	3799 3750	1601 1570	1030 1075	10441 10399	11548 11464	3389 3315	9805 9848	7494 7550	414 <800	1071 1075	105 <800	008> 6	568 <800	9583 9472	321 <800	810 817	2273 2316	304 <800	1721 1688	2872 2857	416 <800	1081 1075	863 879	3642 3620	8901 8850	3982 3958	2980 2965	5978 5938	560 <800	7263 7550	4849 4813
HindIII B9	t t t t	3399	6500	<800	<800	13818	008>		3980	5371	<800	7262	<800	4777	2988	6500	4190	5684	9117	2792	3399	6500	3399	2988	1159	<800	3663	2089	<800	2422	1845	7262	<800	<800	<800
SeqDer		m	<800 6382	: :	<800 449	3383 13872	1	58	1978 4008	1978 5403	<800 121	4742 7032	1356 411	48	<800 2902	65		57	2255 9192		<800 3450		1356 3465	~ ;	<800 1153	49	5430 3478	1543 2041	12275 58	1813 2424		7	35	21	<800 575
ECORI SeqDerMap FngrPrnt		9698	9	, ,	5	3420	1878	880	1945	2022	340		!	6514			4222	1	: :	- 1	Ŋ	7413	1407	2277	089	748	5526	1579	12450	1733	9069	3743	4555	272	59

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only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em. EMBL; Sw., SWISSPROT: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                           Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                   was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                         Group. Further information can be found at this heart ac.uk/HBCyChr9 This sequence is the entire insert of clone RP11-18B16 The true left end of clone RP11-53418 is at 158579 in this sequence. The true right end of clone RP11-168H1 is at 7374 in this sequence. The This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemistry or covered by high quality data (i.e., phred quality) as ditempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-18816 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2672. 2890
/Hote="HAL1b repeat: matches 595. 1751 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2078. .2336
//note="HALlb repeat: matches 109. .397 of consensus"
complement(2205. .2683)
/note="match: GSS: Em:AQ209886"
complement(2220. .2693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note*"MER5A repeat: matches 70. .187 of consensus"
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/note="AluSx repeat: matches 3. .295 of consensus"
4352. 4645
/note="L2 repeat: matches 2816. .3114 of consensus"
6123. 6180
/note="L2 repeat: matches 3202. .3257 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7420. .7549
/note="FLAM_C repeat: matches 2. .132 of consensus"
8109. .8315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER31A repeat: matches 1. .484 of consensus"
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/note="MIR3 repeat: matches 115. .171 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="12 repeat: matches 2808. .3191 of consensus"
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/note="MIR repeat: matches 18. .125 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2389. .2624
/note-"MIR repeat: matches 13. .252 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em: AQ115227"
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/note="match: GSS: Em:AQ197747"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"/db_xref="taxon:9606"
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note="Allogyx repeat: matches 112. .307 of consensus" [4821. .1514]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anotes WILTIK repeat: matches 389. .457 of consensus" 18851. .18963
Anotes L2 repeat: matches 3190. .3313 of consensus" 18964. .19080
Anotes WERIO3 repeat: matches 39. .164 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MLTIK repeat: matches 491. .577 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MLT1H repeat: matches 117. .549 of consensus"
17301. .17600
               8337. .8622

/note="L2 repeat: matches 2958 .3278 of consensus"

8677. .8971

/note="AluY repeat: matches 3. .296 of consensus"

8974. .9274

/note="AluSp repeat: matches 1. .299 of consensus"

9928. .1009

/note="All copies 2 mer aa 65% conserved"

10152. .10373
                                                                                                                                                                                                                                                                                                                                        /note="MLT1J2 repeat: matches 1. .447 of consensus" 11514. 11754 / 11754 / 11040e="1.2 repeat: matches 2635. .2915 of consensus" 11977. 12087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1H repeat: matches 23. .117 of consensus" 17889. .17954
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 3183. .3294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /hote="L2 repeat: matches 2899. .3219 of consensus"
15457. .15770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16389. 16683
/note="Alusx repeat: matches 1. .296 of consensus"
16874. 17300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     // 22079. .22900
/note="L2 repeat: matches 3150. .3268 of consensus"
24230. .24382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MERTA repeat: matches 1. .345 of consensus" (2417, .12427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Alusg repeat: matches 1. .311 of consensus"
16228. .16309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17301. .1700
//note="Alusx repeat: matches 1. .300 of consensus"
17601. .17696
                                                                                                                                                                                                                                                      /note="AluSc repeat: matches 1. .300 of consensus"
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/note="MIR repeat: matches 41. .189 of consensus"

2284. .22511

/note="MIR3 repeat: matches 82. .206 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /notem"AluY repeat: matches 1. .311 of consensus"
14391. .14585
                                                                                                                                                                                                                                                                                                 'note="MIR repeat: matches 28. .129 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR3 repeat: matches 7. .205 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activities of Consensus matches 36. .137 of consensus 20599. .20750
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/note="MIR repeat: matches 61. .210 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andrea MIR3 repeat: matches 7. .154 of consensus*
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'note "MIR repeat: matches 4. .212 of consensus"
                                                                                                                                                                                                 10152. .10373
/note="111 copies 2 mer tc 66% conserved"
10374. .10670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="181 copies 2 mer tc 62% conserved"
20273. .20382
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/note="MIR repeat: matches 48.
22707. .22950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: STS: Em:G03218"
22879, .22988
                                                                                                                                                                                                                                                                               10914
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24383. .24676
/note="AluSq repeat: matches 1. .296 of consensus"
24677. .2478
/note="Milk repeat: matches 9. .61 of consensus"
25049. .25143
/note="L2 repeat: matches 3213. .3312 of consensus"
25126. .25622
/note="L2 repeat: matches 2449. .3000 of consensus"
25577. .25968
/lote="L2 repeat: matches 2961. .3272 of consensus"
26013. .26279
                                                                                                                                                                                                                                                                                                          0; Indels 0; Gaps
                                                                                                                                                                                                  //octe="7.10" repeat: matches 60. 312 of consensus" 26504. 26747 robeat: matches 2337. .2579 of consensus" 26935. 27308 robeat: matches 1. .375 of consensus" 27693. .27866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER3 repeat: matches 140. .202 of consensus" 32750. .32877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 74, .153 of consensus" 32096. .32256
/note="MER3 repeat: matches 1. .140 of consensus" 3257. .3257
/note="Alusp repeat: matches 5. .306 of consensus" 32598. .32516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 19; DB 9; Length 160990; 100.0%; Pred. No. 35; tive 0; Mismatches 0; Indels 0;
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721 GCACAAAACCCAGCTGCAA 739 ô

Db 76321 GCACAAACCCAGCTGCAA 76339

Search completed: August 6, 2002, 20:07:27 Job time: 9651 sec

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AA679456 ac50all.s
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BA799251 HS_45451_B
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AR731923 BNLGH1113
AW141069 EST291092
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W07561 za98h03.r1

BG439573 urvecoso.x

AA199532 mv40a05.r

BF429883 255785 MA

A1005438 uo08005.r

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AA856299 vw99b03.r

T78416 EST5781 Hu

AA856299 vw99b03.r

T78849 vc96h08.r1

AA856299 vw99b03.r

T78849 vc96h08.r1

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BB836241 BB836241
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A2978692 2M0255E11
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BH363397 CH330-48F
BH363397 CH330-48F
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AW312313 4011 MARC
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BB766837 BB786637
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Nagai, M.A. da Silva, W. Jr., Zago, M.A., Bordin, S., Gosta, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Burstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwign.org.br/scripts/gethtml2.pl?ti-&t2-QV3-BTO572-030 200-079-d03st3-2000-02-03st4-1)
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QV3-BT0572-030200-079-d03 BT0572 Homo sapiens CDNA, mRNA sequence.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                        683 GATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAACCCAGCTGCAAACC 742
                                                                                                               623 GTATCCTCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCTG 682
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Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 472 Scd Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                AI654622 384 bp mRNA linear EST 17-DEC-1999 wb48fill.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308941 3',
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BI413457 602987839
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=st2=0V3-BT0572-030
200-079-e01st3=2000-02-03&t4=1)
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922
Tex: +55-11-2704019.
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=0V3-BT0572-030
200-079-c01&t3=2000-02-03&t4=1)
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(bases 1 to 130)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Sllvaw,W. Jr., Zago,M.A., Bordin,S., Costef,F., Garvalho,A.F., Matcukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deolivelra,P.S., Matcukuma,A., Baia,G.S., Simpson,D.H., Bronstein,A., deolivelra,P.S., Metsukuma,A., Baia,G.S., Simpson,D.H., Sangson,A.J. Scares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Shotgun sequencing of the human transcriptome with ORF expressed
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Email: asimpson@ludwig.org.br
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/db_xref="taxon:9606"

/clone_lib="B10572"

/dev_stage="Adult"

/note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                       Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV3-BT0572-030 200-079-g01st3=2000-02-03st4=1)
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukma, A., Baia, G.S., Simpson, D.H., Brunstein, A., Gollveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Ludwig Institute for Cancer Research
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                   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Fax: +55-11-2707001

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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BT0572-030 200-079-a08&t3=2000-02-03&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Fax: +55-11-2707001
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Query Match
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                                     /note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal; Anin-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mkNA and CDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Ondman, G.H., Carvalho, A.F., Matsukuma, A., Bala, C.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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//dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal; Anni-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 / 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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QV3-BEU572-030200-079-b06 BT0572 Homo sapiens CDNA, MRNA sequence.
BE074382
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                               4.8%; Score 36; DB 9; Length 119; 100.0%; Pred. No. 4.3e-08;
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/db_xref="taxon:9606"
/clone_lib="BT0572"
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Best Local Similarity
Matches 36; Conserv
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Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the .minscore 18
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                                                                                                                                                                                                                                                                        EST 25-APR-2001
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Bovidae: Bovinee; Bos.
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Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
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          Length 119;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TP1: 402 762 4366
Fax: 402 762 4390
       DB 9; Le
1.7e-06;
                                                                                                                                                                                                                                                                        mRNA
       4.4%; Score 33; DB 100.0%; Pred. No. 1.7 tive 0; Mismatches
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                                                                                                                                                                                                                                                                     406 bp
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Seg primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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longissimus muscle."
85 c 110 g
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Query Match
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  linear GSS 29-SEP-2000
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Mammalia; Eutheria; Kodentia; Sciurognathi; Muridae; Murinae; Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/5J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
AZ320113 270 bp DNA linear GSS 29-SEP-200 1M0040D004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0040D04 F, DNA sequence.
                                                                                                                                                                                                                                                               1 (bases 1 to 270)
Dural, A. Adyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Adyaqi, A., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wight, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Seq primer: CGTTGTAAAACGACGCCAGT
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University of Utah
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/clone="UUGC1M0040D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0040 row: D column: 04
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Contact: Robert B. Weiss
                                                                                                  AZ320113.1 GI:10371565
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RESULT 11

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 ignated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (dil4732114)[pb]ARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into capators competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
GSS 27-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWN4Inv; Purlfied genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Kodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                        Dunn, D., Agyagi, A., Barber, M., Beacorn, T., Duvai, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                           2M0253G12F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGC2M0253G12"
/clone=ib-Mouse 10kb plasmid UUGC2M library"
/sex-"Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0253 row: G column: 12
                              clone UUGC2M0253G12 F, DNA sequence. AS977289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 6.1
Matches 21; Conservative 0; Mismatches
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 425.
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Fax: 801 585 7177
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State and a state of mena state and state of state subtracted Elmeria tenella cDNA 5. similar to SW.RL22_TRIGR P13732 60S RIBOSOMAL PROPEIN L22 ;, mRNA sequence.
                                                               EST 15-SEP-2000
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                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 912)
                                                                                                 601566052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840829 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.linl.gov Plate: LLCM531 row: h column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-WGC http://mgc.nci.uih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"/db_xref="taxon:9606"
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BE028471.1 GI:8321905
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BE733517
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BE028471/c
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from poly mRNA using an oligo-dT primer containing a Xion site. Following second strand synthesis, EcoRI adapters were ligated to the CDNA and products were size-selected on Sephacryl S600. The CDNAS were ligated to EcoRI/XhoI prepared lambda ZAPII(Stratagene). Clones were converted to phagemids by mass excision using ExAssist helper phage and E.coli SOLR cells (Stratagene). Insert sizes range from 0.7-1.5Kb. The library may contain a small percentage of host or bacterial contaminants. Clones were selected by negative hybridization against a pool of over-represented ESTS (N>-10, from 1506 previous reads)."
                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
Contact David Sibley (toxoest@borcim.wustl.edu) for further
Information relating to organism, libraries, or clone availability.
Trace considered overall poor quality
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Merozoites were obtained from ceacal scrapings of chickens infected with E. tenella. cDNA was synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA linear EST 07-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 456)
Liberator, P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T., Jackson,N., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D. Unpublished (1999)
,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D. WashU-Merck Eimeria tenella project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 bp mRNA linear EST 07-JUN-2 ELESTBED02912.yl Eimeria M5-6 Merozoite stage subtracted Eimeria tenella cDNA 5' similar to SW:RL22_TRIGR P13732 60S RIBOSOMAL PROTEIN L22 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Eimeria M5-6 Merozoite stage subtracted"
/dev_stage="Merozoite"
/lab_host="SOLR E. coli"
                                                                                                Contact: David Sibley, Ph.D. WashU-Merck Elmeria tenella project WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 20; DB 9; Length 358; Best Local Similarity 100.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Eimeria tenella"
/strain="LS18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria tenella.
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Merozolte"
//dev_stage="Merozolte"
//deb_lost="SOLR E. coli"
//note="Vector: Bluescript SK-; Site_l: EcoRI; Site_2: XhoI
: Merozoltes were obtained from ceacal scrapings of
chickens infected with E. tenella. cDNA was synthesized
from poly mRNA using an oligo-df primer containing a XhoI
were ligated to the cDNA and products were size-selected
on Sephacryl SSOO. The CDNAs were ligated to EcoRI/Ahor
prepared lambda ZAPII(Stratagene). Glones were converted
to phagemids by mass excision using ExAssist helper phage
... Folio SOLR cells (Stratagene). Insert sizes range
                                                                                                           Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: -40RP from Gibco.
High quality sequence stop: 427.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and E. Coli SOLR cells (Stratagene). Insert sizes range from 0.7-1.5Kb. The library may contain a small percentage of host or bacterial contaminants. Clones were selected by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               negative hybridization against a pool of over represented ESTs (N>=10, from 1506 previous reads)."
102 c 124 g 116 t 2 others
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1 (bases 1 to 475)
Smith, T. P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 25-APR-2001
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Single pass sequencing. Bases called and alt_trimmed with phred
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                   /clone_lib="Eimeria_M5-6 Merozoite stage subtracted"
/dev_stage="Merozoite"
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                       /strain="LS18"
/db_xref~"taxon:5802"
                                                                                                 est@watson.wustl.edu
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Best Local Similarity 100.0%; Py
Conservative 0;
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BE751494.1 GI:10165486
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                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
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v0.980904.e. Vector identified by cross_match with the -minscore 18
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1 (bases I to 53)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J. Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, aattent and another time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELOLARY DESCRIPTION 1 DESCRIPTION OF THE SECURITY SECURITY SECUENCE. BE75148 MARC 2BOY BOY BOY SECUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. N.C.
                                                                                                                                                                                                                                                                                                                                                                                                              adrenal, and endometrium.
162 c 138 q 82
                                                                                                                                                                                                                                          /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                       Plate: 43 row: F column: 19
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                   /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 43 row: D column: 21
Seg primer: ATTTAGGTGACACTATAG.
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/tissue_type="pooled"
                         and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                        Location/Qualifiers
                                                                                              BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 ATCTTCATCCACTCCCTGGA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                            source
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ΩD
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Smith. T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, J.C., Heaton, M.P., Laegreid, M.W., Rohrer, G.A., Chitko-McKown, C.G., Reele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the .minscore 18
                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
              /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pcMv SPORT6; Site_1: Xba1; Site_2: XhoI: Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary " tothers 124 c 208 g 98 t 1 others
                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                    2.7%; Score 20; DB 10; Length 553; 100.0%; Pred. No. 23;
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100.0%; Pred. No. 23;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454023 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
B1540670
                                                                                                                                                                                                                                                     0; Indels
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TP1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                100.0%; Pred. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
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/tissue_type="pooled"
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Seg primer: ATTTAGGTGACTATAG.
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/lab_host="DH10B"
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578 bp mRNA linear EST 28-NOV-2001 AV614200 Bos taurus adipocyte cell line Bos taurus cDNA clone EIAD003F02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovidae; Bos. 1 to 578)

Takasuga.A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H. and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 19-JUL-2001
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Métazoa: Chordata; Craniata; Vertebrata, Eutèleostomi,
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: p2L1; Site_1: Sal1; Site_2: Not1; Poly A was deleted from a Not1 site"

133 c 209 g 97 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI288757 661 bp mRNA linear EST 19-JUL-2
UI-R-DKO-cde-e-11-0-UI.sl UI-R-DKO Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Bos taurus adipocyte cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 29 (22), E108 (2001)
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21570554
Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Animal Genetics Division
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259 AAGCAGAAGGCCCAGGAAGC 278
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TITLE
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224 AAGCAGAAGGCCCAGGAAGC 243

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Conservative

best Local Similarity Matches 20; Conserved

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/lab_hose="Nath100" (Life Technologies)"
/lab_hose="Nector: pT7T3D-pac (Pharmacia) with a modified
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not 1: Site_2: ECO RI: The UI-R-DKO
polylinker; Site_1: Not 1: Site_2: ECO RI: The UI-R-DKO
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
frue individually tagged normalized rat libraries:
frue individually tagged normalized rat libraries
frue of 20%, heart-RRPP (20%), and placenta-nRPP (20%), and placenta-nRPP (20%), and placenta-nRPP (20%), Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 1, adult day 12, adult day 75, and adult day
adult day 1, adult day 12, adult day 75, and adult day
day 17 RNA and the placenta pool contains only the three
embryonic stages). Bach library was normalized
individually according to the procedure described by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          libraries of brain (CTOS), heart (CSOS), Kidney (CUOS), aorta (CWUS), and placenta (CXOS). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and (CTO), resulting pool of about 10,000 clones represented about 66.5% of the final driver population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria
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                                                                                                                                                                                                                                              Email: msoares@blue.weeg.ulowa.edu
Email: msoares@blue.weeg.ulowa.edu
the sequence contained an oilgo-dr
oilgonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
strand cDNA and therefore tag present in the cDNA between the NoLI site
and the oligo-dr track served to identify it as a clone from the
normalized rat kidney pool library cDNA Library Preparation: M.B.
Scares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: Ml3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DKO subtracted
                                                                                                                                                           451 Eckstein medical Research Building lowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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24;
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                                                                                                                     Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="UI-R-DKO-cde-e-11-0-UI"
/clone_lib="UI-R-DKO"
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illarity 100.0%; Pred. No. 24;
Conservative 0; Mismatches
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TAG_SEQ-CAAGACTGTC"
192 c 185 g 138 t
               Genome Res. 6 (9), 791-806 (1996)
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/db_xref-"taxon:10116"
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                                                                                                      Contact:
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601143045F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506795 5',
        AW914186 690 bp mRNA linear EST 25-MAY-2000 EST345490 Normalized rat brain, Bento Soares Rattus sp. cDNA clone RGAB55 5' end, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 695)
                                                                                                                                                                                 Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                    Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: brain; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: NotI"
1 183 c 184 g 168 t
                                                                                                                                                                                                                                                                    Chandra, I., Mason, T.M., Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nblee@tigr.org
Email: nblee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
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100.0%; Pred. No. 24;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/db_xref="taxon:10118"
/clone="RGIAB55"
                                                                                                                                                                                                                                                                          Lee, N.H., Glodek, A., Chandra, I
Kerlavage, A.R. and Adams, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                     (bases 1 to 690)
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Primer: Oligo dT.

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/organism-"Mus musculus"
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Fax: 301 443 9890
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/lab_host="DH10B" (phage-resistant)"
/note="Yorgan: kidney: Vector: porPar]: Site_1:
/note="Yorgan: kidney: Vector: porpar]: Site_2:
/note="Yorgan: kidney: Vector: porpar]: Vector: Note: Vector: Ve
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602889123F1 NCI_CGAP_Kid14 Mus musculus CDNA clone IMAGE:5044421
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NIH-MGC http://mgc.ncl.nih.gov/.
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             CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM185 row: ) column: 12
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Clone distribution: MGC clone distribution information can be
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Email: cgapbs rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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100.08; Pred. No. 24;
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plate: LLAM11121 row: n column: 06
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/lab_host="DH10B (T1 phage-resistant)"
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Tissue Procurement: DCTD/DTP
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Oligo-driver found, Not I site shown in beginning of sequence oligo-drivers holf found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAS whose availability will be considered under appropriate and limited collaborative arrangements Seq primer: ML3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="vector: pr773D-pec (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NH_BMAP_Ret1_N library is a normalized library derived NHLBMAP_Ret1. NHLBMAP_Ret1 was made from mouse embryonic retina tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu.

TAC_SEC+Non cound"

a 143 c 99 g 85 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UI-M-CCI-bae-d-01-0-UI.sl NIH_BMAP_Retl_N Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                  Caps
Site_2: Sall: Cloned unidirectionally. Primer: Oli
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library. I"
249 c 220 g 151 t
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                      2.7%; Score 20; DB 10; Length 879; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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/db_xref="taxon:10090"
/clone="UI-W-CC1-bae-01-0-UI"
/clone=lib="NIH_BMAP_Ret1_N"
/dev_stage="13.5 days_pc"
/lab_host="DH10B_(Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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/clone_lib-cacolibradiii CC-1690, Lambda Zap II"
/clone_lib-cr. reinhardtii CC-1690, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_I: ECORI; Site_2:
Xhol; This library, constructed by John Davies and Jeffrey
MCDermott, combines CDNas from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark. HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the ECORI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with EXAssist (Stratagene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF418859
UI-R-HJ2-bdj-g-06-0-UI.sl UI-R-BJ2 Rattus norvegicus CDNA clone
UI-R-BJ2-bdj-g-06-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 424)
                                                                                                                        Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J. P., Silliow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Onpublished (2000) Contact: Elizabeth H. Harris DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.5%; Score 19; DB 9; Length 424; 100.0%; Pred. No. 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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                                                                                                                                                                                                                                                                                                                                                                                                  Duke University
Durham, NC 27708-1000, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chlamy@duke.edu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 919 613 8164
Fax: 919 613 8177
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COMMENT
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                                                                                                                                          AUTHORS
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylle, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                  ac50all.sl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:859868 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cloud_lib="Stratagene hnr neuron (#937233)"
/dev_stage="hnr neurons"
/
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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874007G10.xl C. reinhardtii CC-1690, Lambda 2ap II Chlamydomonas
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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100.0%; Pred. No. 71;
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Best Local Similarity 100.0%; Pred. No. /1;
Best Local Similarity 0; Mismatches
          Mismatches
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/db_xref="taxon:9606"
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Fax: 314 286 1810
              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / new_most__niture (this terminity) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 16.5 dpc, the library from which this clone was derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB-UI-R-BJ2
TAG_LIB-UI-R-BJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WGI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/brp/image.html
Insert Length: 721 SGG Error: 0.00
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa: Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 477)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (GGAP),
        The sequence contained an oligo-du track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A trail. The sequence tag present in the cDNA between the NoLI site and the oligo-dT track served to identify it as a clone from the normalized AV canal at 16.5 dpc library CDNA Library Preparation:

M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seg primer: Mi3 Forward
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Email: capabs : Ffmail.nih.gov
Tissue Procurement: Chistopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="IT-R-BJ2-bg1-g-06-0-UI"
/clone="IIb="UI-R-BJ2"
                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
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Email: msoares@blue.weeg.uiowa.edu
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oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message, cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENEFICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 03-OCT-2000
                                                                                                                                                                                                                                                  /note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not 1 - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus Subrayous Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 478)
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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100.0%; Pred. No. 74;
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/clone="UI m~BBAB-avt-a-07-0-UI"
/clone="NIH BMAP_M_S4"
/dev_stage="27-32 days"
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                                                                                                                                                                 /clone="IMAGE:1867520"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH108"
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                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                               High quality sequence stop: 422.
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Seq primer: -40UP from Gibco
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/note="Vector: pBluescript II SK+; Site_I: ECCRI; Site_2:
XhOI; The CDNA library was constructed from mRNA isolated
from the epicotyls of 2 week old seedling for the cultivar
Williams. The seedlings were germinated in a growth
chamber, excised above the soil level, and the plants
were placed in a 100 ppm solution of auxin for 24 hours
prior to harvesting. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT)
sequence with a XhoI restriction site. EccRI adapters
were ligated to the blunt-ended cDNA fragments followed
by XhoI digestion. The CDNA fragments were directionally
cloned into the EccRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This
shoemaker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 09-AUG-1999
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccuéresgen.com High quality sequence stop: 409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS_5451_B1_D11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1027 Col=21 Row=H, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                    /clone="GENOME SYSTEMS CLONE ID: Gm-c1064-3558"
/clone_lib="Gm-c1064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.5%; Score 19; DB 10; Length 481; Best Local Similarity 100.0%; Pred. No. 74; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                           /tissue_type-"seedling epicotyls"
/dev_stage="2 week old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 t
                                                                                                                                                    /organism="Glycine max"
/cultivar="Williams"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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AQ799251
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                                                                                                     FEATURES
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   /lab_host-"DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECC RI; The
NIH BMAP MS 41 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hipoceampus) after a series of subtractions to reduce the
representation of CoNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in Libs process: NIH_BMAP_MS3.1,
NIH_BMAP_MS3.3, NIH_BMAP_MS3.2, NIH_BMAP_MS3.1,
NIH_BMAP_MS3.3, NIH_BMAP_MS3.2, and
NIH_BMAP_MS3.3, NIH_BMAP_MS3.3, NIH_BMAP_MS3.2, and
was used as a driver in a hybridization with a pool of
the NIH_BMAP_MS3.3, NIH_BMAP_MS3.2, and NIH_BMAP_MS3.1
libraries in the form of single-stranded circles (subtracted library)
was purified by hydroxyapatite column chematography,
converted to double-stranded circles (subtracted library)
while bmap_MS3.1 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker, Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B.; Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.5%; Score 19; DB 10; Length 478; 100.0%; Pred. No. 74;
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100.0%; Pic
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BC790803
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LOCUS

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/note="Vector: pBACe3.6; Site 1: ECOR1; Site 2: ECOR1; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Menhylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoLI site and the oligo-dT track served to identify it as a clone from the normalized brown adipose library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 bp mRNA linear EST 17-JAN-2 UI-R-CNI-cjq-g-07-0-UI.sl UI-R-CNI Rattus norvegicus CDNA clone UI-R-CNI-cjg-g-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 Eckstein Medical Research Building Iowa City, 1A 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.5%; Score 19; DB 12; Length 517;
100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                             /clone_lib-"RPCI-11 Human Male BAC Library"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                    /db_xref-"taxon:9606"
/clone="Plate=1027 Col=21 Row=H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CN1-cjg-g-07-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.55, Pred. No. 76;
Best Local Similarity 100.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oliqo-dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                  /organism-"Homo sapiens"
                                                                                                                             High quality sequence stop: 517.
Location/Qualifiers
                                                     row: H column: 21
                         http://www.htsc.washington.edu
plate: 1027 row: H column: 21
Seg primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM386473.1 GI:18186526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 AGTCTCTTCTTGACAATCT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 AGTCTCTTCTTGACAATCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                      BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat
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TITLE
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COMMENT
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ORIGIN
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                                                                                                                                                              FEATURES
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Library made from pooled tissue from day 11, 13, 15, 20,
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                          102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 bp
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High quality sequence stop: 538.
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/db_xref="taxon:29729"
                                                                          168 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                 and 30 embryos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="AKA"
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                                                                                                                                                                                                                                                                                                            442 AGCCTCCTTGGACCTCCTG 460
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium arboreum.
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                                                                                                                                                                                                                                                                                                                                              93 a
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                                                                                                                                                                                                      Query Match
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LOCUS
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                                                                                BASE COUNT
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                                                                                                               ORIGIN
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                  This pool represented 5% of the final driver population.
h) a pool of the 2% most abundant clones in the CNO pool
corresponding to the following addresses: bkw-a-09-0-UI,
bkw-b-09-0-UI, bkw-b-11-0-UI, bkx-b-10-0-UI, bkx-d-06-0-UI, bkx-q-08-0-UI, bkx-h-12-0-UI, bkx-q-06-0-UI, bkx-q-06-0-UI, bkx-h-12-0-UI, bkx-q-06-0-UI, bkx-q-06-0-UI, blx-a-02-0-UI, bkz-d-10-0-UI, bla-a-02-0-UI, bla-q-07-UI, bla-q-07-UI, bla-q-07-UI, bla-q-07-UI, bla-q-07-UI, bla-q-07-0-UI, bla-q-07-UI, bla-q-07-UI, bla-q-07-UI, bla-q-07-0-UI, bla-q-07-UI, bla-q-07-U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 536) Earenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 12-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="vector: pCMv SPORT6; Site_1: Xbal; Site_2: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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ilarity 100.0%; Pred. No. 76;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301304 MAKC 1PIG Sus scrofa cDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRNA
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/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 86 row: M column: 13
Seg primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 g
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TAG_LIB=UI-R-CN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_SEQ=TTGTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           667 CTTCATCCACTCCCTGGAT 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 c
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Matches 19; Conserv
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ORIGIN
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SOURCE

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EST 11-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gossyptimm arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Majolicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossyplum.

1 (bases 1 to 540)
11 (bases 1 to 540)
12 (bases 1 to 540)
13 (bases 1 to 540)
14 (bases 1 to 540)
15 (bases 1 to 540)
16 (bases 1 to 540)
17 (bases 1 to 540)
18 (bases 1 to 540)
19 (bases 
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104 c 119 g 215 t l others
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2.5%; Score 19; DB 10; Length 536; 100.0%; Pred. No. 76; tive 0; Mismatches 0; Indels
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us-10-020-139-1\_copy\_48\_793.oli.rst

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 601.
Location/Qualifiers
                                                                                                                                                    /db_xref*"taxon:10118"
/clone="RG1BB01"
                                                                                                                                       /organism="Rattus sp."
                                                                                               Location/Qualifiers
                                                                            Seq primer: M13 Reverse
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AQ453959.1 GI:4595129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 CTTCATCCACTCCCTGGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear EST 30-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
BNLGH111390 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (297336) hypothetical protein [Arabidopsis thaliana], mRNA
                                                                                                                                         Gossypium hirsutum
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae: Streptophyta; Eucliotyledons; core eudicots;
Rosidae: enrosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 563)
Basewitch, M. Matz.E.C., Davy, D.F. and Burr, B.
ESTs from developing cotton fiber
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.0%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 0; Indels
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/lab_host="XL1-Blue"
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103 c 125 g 222 t
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/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gossypium hirsutum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar≈"Acala Maxxa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 bp
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Brookhaven National Laboratory
Upton, NY 11973, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                          A1731923
A1731923.1 GI:5050775
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                                                                                                                                                                                                                                                                                                                     Contact: Ben Burr
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                                                                                                                                  upland cotton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
Rattus sp.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 21-APR-1999
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Ciones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 741 row: L column: 3
Seg primer: T7
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 601)
                                                                                                                                                                                                                                                                                                                           /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoR1;
Site_2: Not1"
1 152 c 169 q 112 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ453959 601 bp DNA linear GSS 21-APR-HS_5165_B1_F02_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=741 Col=3 Row=L, DNA sequence.
For clone availability, additional sequence and expression information related to this EST please check the TIGR Rat Gene Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a clone contact the ATCC (http://www.atcc.org/atcc.html).
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/clone_lb="RPC1-11 Human Male BAC Library"
/sex="male"
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401 Queen Anne Avenue North, Seattle, WA 98109, USA
TTE1: (206) 616-3819
Fax: (206) 616-3887
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Best Local Similarity 100.0%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 0; Indels
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ORIGIN

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487 CCAGACACACCAGCCTGTT 505
                                                                                                                                                                                                                                                                                             314 CCAGACACCAGCCTGTT 296
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                                                                                                                                                                                            Best Local Similarity 100.0 Matches 19; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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Unpublished (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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1M0243D02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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ECORI Methylase. Size selected DNA was cloned into the
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                                                                                                                                             Query Match 2.5%; Score 19; DB 12; Length 601; Best Local Similarity 100.0\%; Pred. No. 79; Matches 19; Conservative 0; Mismatches 0; Indels
                                                 13 others
                       pBACe3,6 vector at EcoRI sites"
162 c 136 g 164 t
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Insert Length: 10000 Std Error: 0.00
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/db_xref-"taxon:10090"
/clone="UUGC1M0243D02"
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                                                    162 c
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orlifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampioillin resistance. ^{\prime\prime} 154 g 145 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 683)
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2M0164G05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G5PBL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="uUGCZMO164G05"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                     2.5%; Score 19; DB 12; Length 610; 100.0%; Pred. No. 80;
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Insert Length: 10000 Std Error:
Plate: 0164 row: G column: 05
Seq primer: CGTTGTAAAACGACGCCAGT
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University of Utah Genome Center
University of Utah
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated base through a was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase and T4 DNA polymerase bluns end to the blunt ends in high molar excess. The adaptered DNA was purified and size-selected for a 9.5 to
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                                            GSS 27-APR-2001
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                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mussos 1 to 739)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarcers, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                       A2978692
2M0255E11F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0255E11 F, UNA sequence.
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Insert Length: 10000 Std Error:
Plate: 0255 row: E column: 11
Seg primer: CGTTGTAAAACGAGGCCAGT
Class: plasmid ends
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University of Utah
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Contact: Robert B.
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Fax: 801 585 7177
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Matches 19; Conserva
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purified. The sheared, adaptored mouse DNA was annealed to
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                       adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

162 c 160 g 165 t lothers
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Vukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 694)
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Seg primer: M13 Reverse
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/note-"Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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100.0%; Pred. No. 82;
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Tel: 301 838 0200
Fax: 301 838 0208
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Department of Eukaryotic Genomics
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/Glono="2024G22"
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Other_GSSS: CIT-HSP-2024C22.TF
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 19; Conservative
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es 19; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI829148 796 bp mRNA linear EST 04-OCT-200 603079250F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5170885 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 796)
NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM11425 row: c column: 14
                                                                                                                                                                                                                                                                                                                                                                                             /clone="GA_Eb0023B01f"
/clone_lib="Gossypium arboreum 7–10 dpa fiber library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI" 161 c 155 g 298 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11206143.
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 19; DB 10; Length 782;
100.0%; Pred. No. 86;
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                                                                                           Clemson Universitý
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4298
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                       /organism="Gossypium arboreum"
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/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
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                                                                                                                                                                                   Email: rwing@clemson.edu
Seg primer: TAATAGGACTGATATAGGG
High quality sequence stop: 761.
Location/Qualifiers
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100.0%; Pic
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BI829148/C
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                                                                       EST 07-MAR-2001
                                                                                                                                                                                                                                                                                                                                              Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11206145.
Contact: Wing RA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids II; Malvales, Malvaceae, Gossypium.
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                  BF275075
GA_Eb0023B03f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Eb0023B03f, mRNA sequence.
                                                                                                                                                                                                                                  Gossypium arboreum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:29729"
/clone="GA_Eb0023B03f"
/clone_lib="Gossypium_arboreum_7-10_dpa_fiber_library"
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161 g 295 t
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100 Jordan Hall, Clemson, SC 29634, USA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rwing@clemson.edu
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                                                                                                                                                                  BF275075.2 GI:13248287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 864 656 7288
Fax: 864 656 4293
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ORIGIN
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                             RESULT 41
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100.0%; Pred. No. 88;
ive 0: Mismatches 0; Indels
                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CHORI-230 Segment 1"
                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                            828 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="BN/SsNHsd/MCW"
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/clone="CH230-48F10"
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                                                                                                                                                            BH363397.1 GI:17294131
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B1462868
B1462868.1 GI:15253524
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Matches 19; Conserv
                                                                                                                                                                                                           Norway rat
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                                                                            BH363397
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                                                      BH363397/C
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AUTHORS
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anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIHMC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 07-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Mosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (Dases 1 to 845)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, W.D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium arboreum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GA__Eb0023M18f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: xhol"
172 c 175 g 313 t. 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11206414.
Contact: Wing RA
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                                                                                                                                                                                                                                             2.5%; Score 19; DB 10; Length 796; 100.0%; Pred. No. 86; ulive 0; Mismatches 0; Indels
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Pred. No. 88;
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High quality sequence stop: 798.
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/db_xref="taxon:29729"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
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100.0%;
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
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BF275344/C
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M. Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other GSSs: CH230-48F10.TJ
                             CH230-48F10.TVB CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-48F10, DNA seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
GSS 03-DEC-2001
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/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoR1;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 48 row: F column: 10 Seg primer: T7
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Genome Res. 10 (10), 1617-1630 (2000)
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ITOh,M., Konbo,H., Okazaki,Y., Muramatsu,M. and Haysahizaki,Y.
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (strain:C57BL/6J) adult male hippocampus cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2900073M23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        licity of the selected for average insert size 2.2 km and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NMCR1, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                               Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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                                                                                                                                                                                                                   CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIGO row: e column: 14
High quality sequence start: 3
High quality sequence stop: 628.
              1 (bases 1 to 1095)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1MAGE:5273461"
                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_97"
/lab_host="DHl08"
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Sadoth, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaqaki, T., Hara, A., Hayatsu, N. Hill, D., Hiranoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawa, M., Koya, S., Kato, H., Kawa, M., Koya, S., Kato, H., Kawa, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, S., Salto, R., Sakai, K., Sano, H., Sasaki, D., Schin, L., Shibata, K., Shibata, Y., Shinaqawa, A., Shiraki, T., Tanaka, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physical and Chemical Research (R.KEN). Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute: 1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Managawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Shibata,K. Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., 1shii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakquchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira, A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Nature 409, 685-690 (2001)
5 (bases 1 to 2343)
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AA980784 152 bp mRNA linear EST 27-MAY-1998 ua45e12.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1349710 5', mRNA sequence.
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                                                                                                                                                                                                      GOESLEAVAQRLELREVTYFSI,MYYNKQNQRRWVDLEKPLKKQI,DKHALEPTVYFGVL
                                                                                                                                                                              /translation-"MPLPFGLKLKRTRRYTVSSKSCLVARIQLLNNEFVEFTLSVEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 152)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llul.gov) for further information.
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                                        protein tyrosine phosphatase, non-receptor type 21 putative"
source: MCD, source key: MGI:1344406,
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/sex="male"
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WashU-HHMM Mouse EST Project
Washington University School of MedicineP
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2.5%; Score 19; DB 1
Best Local Similarity 100.0%; Pred. No. 1.2e
Betches 19; Conservative 0; Mismatches
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/db_xref*"G1:12851270"
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/db_xref="taxon:10090"
/clone="IMAGE:1349710"
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/lab_host="DH108"
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Fax: 314 286 1810
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Konno, H., Atawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Haro, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, J., Kaiy, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kando, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, Y., Miki, Mizuno, Y., Namanura, T., Shipata, Y., Shipamoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Y., Yano, Y., Watahiki, A., Watanabe, S., Yanamura, T., Yamanaka, T., Yano, Y., Yanamura, T., Yamanaka, T., Yano, M., Muramatsu, M., and Hayashizaki, Y., Shibai, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y., Unpublished (2000)
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URL:http://genome.go.gc.riken.go.jp,
Carninci,P., Nishiyama,Y., WestoverA., Itoh,M., Nagaoka,S., Sasaki
'N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                    EST 25-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB055152 RIKEN full-length enriched, 12 days embryo male wolffian duct Mus musculus CDNA clone 6720477907 3's similar to AF071314 Mus musculus COP9 complex subunit 4 (COPS4) mRNA, mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 239)
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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O
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100.0%; Pred. No. 1.8e+02;
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Best Local Similarity 100.08; Pred. No. 1.00
Oneservative 0; Mismatches
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                                                                                                                                                                                                                                                           47 9
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BB055152.1 GI:8462300
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primer [5'
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double-stranded cDNA was size selected. ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 25-FEB-2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s. Wiemann@dKf2- heidelberg.de; sequenced by DKF2 (German Cancer Research Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL119042 275 bp mRNA linear EST 25-FEB-DKF2p761P17121_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKF2p761P17121 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 275)
Poustka, A. Klein, M. Mewes, H.W., Gassenhuber, J. and Wiemann, S. Epr (Poustka, et al.)
Unpublished (1999)
Contact: Poustka A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heubnerweg 6, 14059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Inhestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
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/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: poustka@mpimg-berlin-dahlem.mpg.de
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Best Local Similarity 100.0%; Pred. No. 2.1
                                                                             /organism="Mus musculus"
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     High quality sequence stop: 238.
                                                                                                     /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda I. Cloning sites, 5' end: SalI; 3' end: BamHI" 45 c 45 c 973 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marka,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                         /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                    /tissue_type="wolffian duct includes surrounding region"
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA062149

mj85f04.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:482911 5' similar to SW:RPOM_YEAST P13433 DNA-DIRECTED RNA
POLYMERASE MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
                                                                                                                     /clone="6720477P07"
/clone_lib="RIKEN full-length enriched, 12 days embryo
male wolffian duct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE Consortium (info@image.linl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.4%; Score 18; DB 9; Length 239; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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Seg primer: -28M13 rev2 from Amersham
                                                  /organism="Mus musculus"
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                                                                                               /db_xref="taxon:10090"
  Location/Qualifiers
                                                                          /strain~"C57BL/6J"
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                                                                                                                                                                                               /sex="male"
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Fax: 314 286 1810
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us-10-020-139-1\_copy\_48\_793.oli.rst

BASE COUNT

Matches

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1. .296 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 239.
Location/Qualifiers
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                                                                                              W36972.1 GI:1318358
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314 286 1810
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                                                                                              VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing, Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia: Futheria: Cetarticaactyla: Suina: Suidae: Sus. Preking B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                             Gaps
                                   /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
62 c 58 9 68 t 1 others
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                                                                                                                                   2.4%; Score 18; DB 9; Length 275; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                              276 bp mRNA linear 4011 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence. AW312313 AW312313.1 GJ:6728183 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 18; DB 9; Le Local Similarity 100.0%; Pred. No. 2.1e+02; Les 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Sus scrofa"
/db_xref-"taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib-"MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host="DH108"
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1. .276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 g
/dev_stage="adult"
/lab_host="DH108"
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                                                                                                                                                                                                                     246 AGAAATTGCTGAACAATG 263
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                                                                                                                                                           Best Local Similarity
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BASE COUNT

FEATURES

Matches

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

RESULT 52

PP ò

AW312313

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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[ (bases 1 to 296)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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EST 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was size selected, ligated to Eco RI adapters. (Phermacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF290469 321 bp mRNA linear EST 28-NOV-20 EST455060 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIHV92 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
W36972 296 bp mRNA linear EST 11-SEP-19
mmb75c10.r1 Soares mouse p3NMF195.5 Mus wusculus CDNA clone
IMAGE:335250 5' similar to SW.RPOM YEAST P13433 DNA-DIRECTED RNA
POLYMERASE MITOCHONDRIAL, PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
WashJ-HHMI Mouse EST Project
WashJ-HHMI Mouse EST Project
WashJ-HMI Mouse EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.4%; Score 18; DB 10; Length 296; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
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Rattus norvegicus
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/organism-"Homo sapiens"

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Query Match
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Chris Moskluk, M.D., Ph.D., Michael R.

Tissue Procurement: Chris Moskluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="vector: pT3T7Pac; Site_1: Ecokl; Site_2: Not1; Combination of ROV, RBR, RKI, RLI, RPL, RLU, REM, RMU, RSP, RHE, RPC, RPN"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                          Pertea, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hB3h02.yl NCI_CGAP_GUI Homo Sapiens CDNA clone IMAGE:2969427 5' similar to TR:075139 075139 KIAA0644 PROTEIN. ;, mRNA sequence. AW662992
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10116"
/clone="RcHHV92"
/clone_lib="Rat Gene Index, normalized rat, Rattus
norvedfcus cDNA"
                                                                                      Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pert Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares
                                                                                                                                                                                                                                                                                                           This close is available through the ATCC, contact the ATCC tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                     Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
1711, Medical State (1910) - 838 - 3529
Fax: (301) - 838 - 0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LINL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
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1. .323
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Unpublished (1997)
Other_ESTs: hh83h02.x1
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                                                                       (bases 1 to 321)
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Best Local Similarity
Matches 18; Conserv
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Ishikawa, T., Hara, A., Hayatsu, N., P., Endo, T., Ishikawa, T., Ishikawa, T., Itoh, M., Hirozane, T., Hori, F., Ishi, Y., Kaya, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Atsuyama, T., Mki, Y., Maruno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Y., Yano, R., Yasunishi, A., Yokota, T., Yamanza, T., Yamanza, T., Yamanza, M., Muramatsu, M. and Hayashizaki, Y., Shino, W., Wamanza, M., Hayashizaki, Y., Unpublished (2000)
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1988)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB491192 RIKEN full-length enriched, 13 days embryo stomach Mus musculus cDNA clone D530019N12 3' similar to AF071314 Mus musculus COP9 complex subunit 4 (COPS4) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 323)
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Carning, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, High-efficiency full-length cDNA cloning.
                                                                                                                                                                                                             /note-"Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. primer: Oligo dT. Library constructed by Life Technologies."
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                                                                                                  /tissue_type="2"pooled high-grade transitional cell tumors"
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                                       /clone="IMAGE:2969427"
/clone_lib="NCI_CGAP_GU1"
/db_xref-"taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                6 d
                                                                                                                                                                                          /lab_host="DH10B"
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BB491192.1 GI:9449819
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Mus musculus
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Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R. Moon, E.P., Kim, M.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear EST 20-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                           prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Orýzeae: Orýza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA751893
96AS0752 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa
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University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seg primer: M13 Reverse Primer.
                                                                                                                                                                                                                                   /note="Site] Sall; Site_2: BamHI; CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken project of Genome Exploration Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                               /clone_lib~"RIKEN full-length enriched, 13 days embryo
stomach"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
          please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%; Score 18; DB 9; Length 323;
100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                               /Lissue_type="stomach"
/dev_stage="13 days embryo"
/lab_host-"DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
                                                                                        /organism="Mus musculus"
                                                                                                             /db_xref = "taxon:10090"
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                                                   Location/Qualifiers
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Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 GCTTTGGAAACTTGTTCT 206
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Best Local Similarity 100.0
Matches 18; Conservative
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                                       further details.
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19-44 (1999)
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/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 335)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Hillier,L., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear EST 25-NOV-1997
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                     /note="Vector: pBluescript SK(+); Site_1: EcoR1: Site_2: Xho1: Directional CDNA library inserted into lambda ZAPII vector at 5'end with EcoR1 and 3' end with Xho I site."
/cultivar="Milyang23"
/db_xref="taxxon:4590"
/clone="96A8752"
/clone=lib="Rice Immature Seed Lambda ZAPII cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      v102a07,r1 Soares_mammary_gland_NbWMG Mus musculus cDNA clone
IMAGE:964964 5' similar to SW:RPOM_YEAST P13433 DNA-DIRECTED RNA
POLYMERASE MITOCHONDRIAL PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3']; double-stranded cDNA was ligated to Eco RI
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                          Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 18; DB 9; Length 332
100.0%; Pred. No. 2.3e+02;
lve 0; Mismatches 0; Indels
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                                                                                                             /tissue_type="lmmature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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High quality sequence stop: 292.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monseest@watson.wust).edu
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/clone="IMAGE:962964"
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Best Local Similarity 100.0%;
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Fax: 314 286 1810
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/organism="Mus musculus"

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Query Match
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URL:http://genome.gsc.riken.go.jp,
Carninoi,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
O., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
DOMAN Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y., and Hayshizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB224526 IKEN full-length enriched, adult male acrta and vein Mus musculus cDNA clone A530086622 3' similar to NM_001706 Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6) mRNA, mRNA
adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p17T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system. Genome Res. 9 (5), 463.470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Automated filtration-based high-throughput plasmid preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                  Length 335;
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                                                                                                                                                                                                                                                                            2.4%; Score 18; DB 9; Le
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                            80 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB224526.1 GI:8893138
                                                                                                                                                                                                                                                                                                                                                                                                           667 CTTCATCCACTCCCTGGA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 CTTCATCCACTCCCTGGA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                                                                                                                                            116 c
                                                                                                                                                                                                                                                                                                               Local Similarity 100.0 ies 18; Conservative
                                                                                                                                      Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednence.
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 59
                                                                                                                                                                   BASE COUNT
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Location/Qualifiers

further details.

source

FEATURES

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Adams, N.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult (J. Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White (C.J., Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White (C.J., Lee, N. H., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Tr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Pelligrino, S.M., Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Sangla, M., Coleman, T.A., Collins, E.J., Bednarik, D.P., Goo, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S.; Olsen, H., Raymond, L., Wei, Y.E., Whig, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA350438 336 bp mRNA linear EST 21-APR-199 EST57699 Infant brain Homo sapiens CDNA 5' end similar to similar to ankyrin, brain, mRNA sequence.
                                                                                                                                                                                                                                          /note="Site_1: Sal1: Site_2: BamH1: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                        /clone_lib="RIKEN full-length enriched, adult male aorta and vein"
                                                                                                                                                                                                                                                                                                                                                                     RIKEN. Division of Experimental Animal Research in Riken
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100.0%; Pred. No. 2.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                    /tissue_type="aorta and vein"
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/db_xref="taxon:10090"
/clone="A530086P22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 9
                                                                                                                                                                                            /dev_stage="adult"
                                                                                                                                                                                                                   /lab_host-"DH10B"
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                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 CIGCAGAAGGAGATAIGT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 c
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1 (Dases 1 to 34)

S Adams, M.D., Kerlavage, A.R., Fleischmann, B.D., Fuldner, R.D., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Fischer, C., Hasings, G.A., He, W.W.,

HH, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Fischer, C.M., Dillion, P.J., Fannon,

M.R., Kosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
/dev_stage="34 years old"
//deb_nost="%3ClR (kanamycin resistant)"
//deb_nost="%3ClR (kanamycin resistant)"
//deb_nost="%3ClR (kanamycin SK-; Site_1: EcoRI: Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4%b.
Mateerial obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
KNAS from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI372485 343 bp mRNA linear EST 12-JA EST175320 Infant brain, Bento Soares Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: HGI (Human Gene Index)
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: EST175319 EST175321 EST175322 THC290418
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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/clone_lib="Infant brain, Bento Soares"
/lab_host="E. coli DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.4%; Score 18; DB 9; Le Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"/db_xref="taxon:9606"
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A1372485.1 GI:4152351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AGAAATTGCTGAACAATG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 AGAAATTGCTGAACAATG 339
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Fax: (301)-838-0208
Email: hgi@tigr.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
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COMMENT
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Homes 1 to 341)

Hillier, L., Allen, M., Howles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, H., Schellenberg, K., Steploe, M., Tan, P., Theising, B., While, Y., Wylie Washu-Merck EST Project 1997,
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                        Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="infant"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NoII" 76 g 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-tree through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA285185
zs60b06.rl Stratagene schizo brain SII Homo sapiens cDNA clone IMAGE7701843 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.4%; Score 18; DB 9; Length 336; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Stratagene schizo brain Sll"
/sex="male"
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/db_xref="taxon:9606"
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                                                                     Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:701843"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 308.
         Other_ESTs: EST57698 THC173165
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AA285185.1 GI:1928148
                                             Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AGAAATTGCTGAACAATG 98
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Fax: 314 286 1810
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Best Local Similarity
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Mylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                359 bp mRNA linear EST 11
MAGE:336673 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                        Score 18; DB 12; I
Pred. No. 2.3e+02;
                                      100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:336673"
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The WashU-HHMI Mouse EST Project
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Location/Qualiflers
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                                                                                                                162 TCCTTGAGAACTGAAGG 179
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                                                                                                                                           41 TCCTTGAGAACTGAAGG 24
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Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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EcoRI: Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a compination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BHOB electrocompetent cells (BRL Life Technologies).

102 c 107 g 10 thers
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Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jone
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 271 row: B column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Anote="Vector: BA, MI3-derived; Site_1: HindIII; Site_2: Not1; The infant brain library, constructed by Bento Soares, Columbia University, was oligo (dT) primed and directionally cloned into an MI3-derived plasmid using total brain mRNA from a 72-day old human female afflicted with spinal muscular atrophy. "
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 351)
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RPCI-23-271B8.TJ RPCI-23 Mus musculus genomic clone RPCI-23-271B8,
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                               2.4%; Score 18; DB 9; Length 343; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) Other_GSSs: RPCI-23-271B8.TV
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/strain="C57BL/6J"
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/clone="RPCI-23-271B8"
/clone_lib="RPCI-23"
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                                    EST 20-FEB-1995
                                                                                                                                                                                                          Auffray, C., Behar, G., Bols, F., Bouchier, C., da Silva, C., Devignes, Auffray, C., Behar, G., Bols, F., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, Y., Pietr, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A. IMAGE: molecular integration of the analysis of the human genome
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Mammalia; Eutheria; Primutes; Catarrhini; Hominidae; Homo.
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                                                 HSC18G111 normalized infant brain cDNA Homo sapiens cDNA clone
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Seq primer: (-21)M13_universal.
Location/Qualifiers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                        and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _lib="normalized infant brain cDNA"
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nes 0;
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                                    mRNA
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                                361 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genexpress@genethon.fr
                                                                        c-18g11, mKNA sequence.
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                                                                                                       F06455.1 G1:672030
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                                                                                        F06455
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                                                   DEFINITION
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                                                                                                                                                             ORGANISM
   RESULT 65
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SOURCE
                                                                                        ACCESSION
                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                          MEDLINE
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                                                                                                                          KEYWORDS
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EST 12-MAR-2001
                    1 (bases I to 369)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
Hillier,L., Rohlfing,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
Y.R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDHH19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae: Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 bp mRNA linear EST 12-MAR-2
UI-R-CSO-bti-e-09-0-UI.sl UI-R-CSO Rattus norvegicus cDNA clone
UI-R-CSO-bti-e-09-0-UI 3', mRNA sequence.
BG379573.1 GI:13304045
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 TFE: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="19 weeks" /
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib~"Soares_fetal_lung_NbHL19W"
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 18; DB 10; I
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: mob.REGA+ET
High quality sequence stop: 239.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GDB:1245553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:300629"
                                                                                                                                                                                                                                                                                                                    est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 18, Conservative
                                                                                                                                                                    Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
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//dev_stage="AbULT"
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                     The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first trans to bond and therefore this may represent a bonafide poly a tail. The sequence tag present in the cDNA between the NoII stand the oligo-dT track served to verify it as a clone from the normalized rat heart pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                 451 Ecks.ein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref=ftaxon:10116"
/clone="UT-R-CSO-bti-e-09-0-UI"
/clone_lib="UT-R-CSO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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TAG_TISSUE=rat heart pool
TAG_SEQ=ATAAGATAAC"
                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Forward
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AA199532.1 GI:1794835
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University of Iowa
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EST 29-NOV-2000
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A survey of genes transcribed in bovine skeletal muscle Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adaptics (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 375)
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                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Bento Soares and M. Fatima Bonaldo.
69 c 88 g 102 t
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%; Score 18; DB 9; Length 374;
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4399
                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:657488"
/clone_lib="Soares mouse 3NME12 5"
                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                              Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                       High quality sequence stop: 349.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACKWARD: GITITCCCAGICACGAC
                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                 /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 CTCAGAGICTCTTGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 CTCAGAGTCTCTTCTTGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                            MGI:403336
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 380)

Sadams, M. D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N., Kirkness, E.F., Brandon, R.C., Chiu, M. W., Clayton, R.A.,

Cline, R. T., Cotton, M. D., Earle-Hughes, J., Fine, L.D., FitzGerald

L.M., FitzBudh, M.M., Fritchman, J.L., Geoghagen, N.S.M., Glock, A.,

Gnehm, C.L., Hanna, M.C., Heddlom, E. Hinkladr, P.S., Kelley, J.M.,

Klimek, K.M., Kelley, J.C., Liu, L. T., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pellegrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Endnarik, D., Feng, P., Ferrie, A., Utterback, T.R., Weldman, J.F., Li, Y.,

Bednarik, D., Feng, P., Ferrie, A., Eischer, C., Hastings, G.A., He, M.-M.,

Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei

Y. F.F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon

Wenter, J.C.
                                                                                                                                                                                                       T33416 380 bp mRNA linear EST 06-SEP-1995 EST57781 Human Brain Homo sapiens cDNA 5' end similar to None, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence Nature 377, 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="ATCC (inhost):104057"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Human Brain"
/note="Organ: brain"
75 c 95 g 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: EST57780
                 411 GGCCCATCATTGGCCAGA 428
                                               314 GGCCCATCATTGGCCAGA 331
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Matches 18; Conservative
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                                                                                                                                                                            /note="vector: Uni-ZAP XR; Site_1: EcoR1: Site_2: XhoI; Library obtained from Stratagene, catalog #937721. Library made from skeletal muscle of a two year old Holstein cow." 101 93 g 117 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI'CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 601 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.4%; Score 18; DB 10; Length 375; Best Local Similarity 100.04; Pred. No. 2.3e+02; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-lib-"Soares_NFL_T_GBC_S1"
                                                                                                                                  /tissue_type="Skeletal muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soares and M. Fatima Bonaldo.
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High quality sequence stop: 352.
Location/Qualifiers
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/db_xref-"taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 bp
                                         /organism="Bos taurus"
/db_xref~"taxon:9913"
/clone_lib="MARC BSM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 9
Location/Qualifiers
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                                                                                                                                                          /lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI005438
AI005438.1 GI:3214948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 CAGCCAAATCATCAACAA 585
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Unpublished (1997)
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Gaps

0

Indels

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Mus musculus
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Hus.
1 (bases 1 to 382)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 07-MAR-1995
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:368684"
/clone_lib="Soares mouse embryo NbMEl3.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/63"
                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 293.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 CTTCATCCACTCCTGGA 325
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Matches 18; Conservative
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                             house mouse.
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                                                                                                                                                                           Mus musculus

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheria; Rodentia; Sciurognathi; Muridae; Murnae; Mus.

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3']; double-stranded cDNA was ligated to Ecc RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTyT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento a 135 c 484 g 72 t.
  EST 09-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                      vw99b03.rl Soares_thymus_2NbMT Mus musculus cDNa clone
IMAGE:1263053 5' similar to TR:000411 000411 MITCCHONDRIAL RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU HHMI Mouse EST Project.
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%; Score 18; DB 9; Length 381; 100.0%; Pred. No. 2.4e+02; Live 0; Mismatches 0; Indels
linear
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mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouseest@watson.wustl.edu
381 bp
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/clone="IMAGE:1263053"
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                                                          POLYMERASE. ; , mRNA sequence.
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                                                                                                         AA856299.1 GI:2944601
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W56936.1 GI:1358814
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Best Local Similarity 100.0
Matches 18; Conservative
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AA856299
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/lab_host="PH10B (ampicillin resistant)"
/lab_
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Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
l (bases l to 390)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rikin, L., Roblfing, T., Sobres, M., Tan, F., Trevaskis, E., Waterston
, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
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Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 2023
High quality sequence stops: 342 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.lhnl.gov) for further information.
Insert Length: 2023 Std Error: 0.00
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A054P39U Hybrid aspen plasmid library Populus tremula x Populus
tremuloides cDNA 5', mRNA sequence.
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels 0; Gaps
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/clone_lib="Soares infant brain lNIB"
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/db_xref="GDB:396313"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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Seg primer: M13RP1
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Matches 18; Conservative
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Fax: 314 286 1830
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                                                                                                          Department of Biotechnology
Royal Institute of Technology (KTH)
Technikringen 34, S-100 44 STOCKHOLM, Sweden
TTel: +46 8 790 8287
Fax: +46 8 24 54 52
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gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastrointestinal tract or pancreas, Sjorgen's syndrome, graves disease, thyroiditis, insulin-dependent diabetes, pencreatitis, ulcerative colitis, Crohn's disease and atrophic gastritis. Host cells containing expression vectors comprising the HPSP mucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to PHSP-expressing cells, to detect cells that express HPSP, to monitor patients being treated with HPSP, and for purification of HPSP from natural sources. Expression of HPSP may to detect the detect the provider antiponing sequences (optionally after amplification by PCR) by hybridisation, particularly for diagnosis and monitoring of disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 caaaggeettaaeetgagetteeetgteaeegegaatgteaetgtggeegggeeeateat 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 cateteaettteettgetggacaaacacagecaaateateaacaagttegtgaatagegt 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 cgacctaggagtgcttcagaaatccagtgcttggcaactggccaagcagaaggcccagga 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 agetgagaaattgetgaacaatgteatttetaagetgetteeaactaacacggacatttt 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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treat cancer and autoimmune diseases particularly of secretory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19; Length 824;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        but also for mapping the chromosomal sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                                                                                                                                                      Parotid secretory protein; hPSP; digestive disorder; endocrine disorder;
                                                                                                                                                                                                                                                                                                                                                                     non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1028 BP; 274 A; 299 C; 222 G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                      Human parotid secretory protein coding sequence.
767 gcacaaaacccayctgcaaaccctca 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                              AAV44759 standard; DNA; 1028 BP
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/product= hPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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103..795
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                                                                                                                                                                                                                                                                                                                                                                                              therapy; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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Gaps

0;

100.0%; Score 746; DB 19; Length 1028; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0;

Best Local Similarity 100. Matches 746; Conservative

Query Match

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301 TGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATGATGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 TGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCAAATTGAAAC 480
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                               48 gatgettcagetttgggaaacttgttetectgtgeggggggeteactggggaeetcagagtc 107
                                                                                                                   61 TCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120
                                                                                                                                                                                                                                   121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGT 180
                                                                                                                                                                                                                                                                     181 CGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                           228 egaectaggagtgetteagaaateeagtgettggeaactggeeaageagaaggeeeagga 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AGCIGAGAAATIGCIGAACAAIGICATITCIAAGCIGCIICCAACIAACAGGACAITIT 300
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                                                                                                                                                                        108 tettettgacaatettggcaatgacetaagcaatgtegtggataagetggaaeetgttet 167
1 GAIGCTICAGCTIIGGAAACTIGIICICCIGIGCGGGGGGGGTGCICACIGGGACCICAGAGIC 60
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neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
hypothalamic disorder; glandular disorder; macrophagal disorder;
epithelial disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immunologic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO1025 nucleotide sequence SEQ ID NO:37
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181 CGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Discretal and certified by the compounds include bengin or malignant tumours antibodies and other compounds include bengin or malignant tumours (e.g., renal, liver, Kidney, bladder, breast, gastric, ovarian, conficient, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stronal and blastocoelic disorders, and inflammatory, primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58167 to AAC5836 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO6199, PRO1017, PRO8099, PRO8199, PRO1107, PRO1101, PRO1105, PRO11089, PRO1059, PRO10107, PRO11011, PRO1153, PRO1182, PRO1184, PRO1187, PRO1281, PRO23, PRO839, PRO834, PRO81117, PRO1710, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 tettettgacaatettggcaatgacetaagcaatgtegtggataagetggaacetgttet 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard A, Gurney AL, Hillan KJ, Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 1049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 1049 BP; 279 A; 299 C; 236 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 746; D
100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                                                   99WO-US12252.
99US-0141037.
99US-0143048.
99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                99WO-US28313.
99WO-US30911.
                                                                                                                                                                 06-JAN-2000; 2000WO-US00376.
                                                                                                                                                                                                                              99WO-US05028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 746; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
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                                                      WO200053755-A2
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   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        26-JUL-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe CK,
                                                                                                                                                                                                                              08-MAR-1999;
                                                                                                                                                                                                                                                      02-JUN-1999;
23-JUN-1999;
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                                                                                                             14-SEP-2000.
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Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis, hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
                                                                               360
                                                                                                                                                                                                                                                                                                                             540
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                                                                                                                                                                                                                                                                 426 caaaggeettaacetgagetteeetgleacegegaatgteaetgiggeegggeeeateat 485
                                                                                                                                                                                                                                                                                                       TGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAAC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 CCGCATCTTCATCCACTCCTGGATGTGAATGTCATTCAGCAGGTCGATGATCCTCA 720
                 246 cgacctaggagtgcttcagaaatccagtgcttggcaactggccaagcagaaggcccagga 305
                                                                                                                                        Human secreted protein encoding cDNA SEQ ID #26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 GCACAAAACCCAGCTGCAAACCCTCA 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA87727 standard; cDNA; 1058 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               septic shock; impotence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200037491-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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This sequence represents human cDNA encoding a secreted protein. The invention relates to sequences AAA87725-A87774 which encode human secreted proteins a secreted proteins and secreted proteins and secreted proteins include signal peptides. Included in the invention are a host call containing one of the cDNA sequences, and a purified antibody capable of blinding to one of the secreted proteins. Also conductained in the invention are methods for secreted proteins and a method for the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapphing procedures and may be used to creat diseases including cancer, autoimmune diseases, cardiovascular disorders, eyellisories, whypothyroidism, immunological disorders, obesity, mitochondriosytopathies, diabetes, atherosclerosis, considered and secretics of the invention and includences are selected may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriosytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, and a service of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGGAGAGAGGCCCAGGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 teacgagggaettgagacagttgacaatactettaaaggcateettgagaaaetgaaggt 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 gatgetteagetttgggaaaettgtteteetgtgeggegtgeteaetgggaeeteagagte 125
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                                                                                                                  Polynucleotides and polypeptides encoding proteins with signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dementia, hyperlipidaemia, septic shock and impotence.
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100.0%; Pred. No. 0;
                                                                                                                                             in diagnostic, forensic,
                                                                                                                                                                                                                                         Claim 1; Page 163-164; 306pp; English.
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                       WPI; 2000-442637/38.
                                                                                                                                                                                   mapping procedures
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                                                         P-PSDB; AAB25765
                                                                                                                                                    peptides, useful
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121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGT 180
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100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                      cDNA encoding human secreted protein #10.
                                                                                             721 GCACAAACCCAGCTGCAAACCCTCA 746
                                                                                                                     786 gcacaaaacccagctgcaaaccctca 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 221; 307pp; English.
                                                                                                                                                                               AAF64009 standard; cDNA; 1058 BP
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                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2000; 2000WO-IB00951.
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                                                                                                                                                                                                                              05-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-071487/08.
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                                                                                                                                                                                                                                                                                                                                         W0200100806-A2.
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                      AAF64009
                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 caaaggeettaacetgagetteeelgteacegegaatgteaetgtggeegggeeeateat 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 tgatccccagacacaccaccagcctgttgccgtcctgggagaatgcgccagtgacccaaccag 605
             gene therapy and chromosome
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61 PCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120
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                                                                                                                                                                                                                                                                                                                            661 CCGCATCTTCATCCACTCCTGCATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCA 720
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                                                                               606 cateteaettteettgetggacaaacamagecaaateateaacaagttegtgaatagegt 665
                                                                                                                                                              GAICAACACGCIGAAAAGCACTGIAICCTCCTGCIGCAGAAGGAGAIAIGICCACIGAI 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGGGGCGTGCTCACTGGGACCTCAGAGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 49 Secreted proteins and the CDNAS
                                                                                                                                                                                                          541 CATCICACTITCCTIGCTGGACAACACCCAAATCATCAACAAGTICGTGAATAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; prevention; treatment; diagnosis; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1058 BP; 291 A; 302 C; 231 G; 234 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards J, Bouqueleret L, Jobert S;
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neuroprotéctive; antidepréssant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muladi.
antiinflammatory; antirheumatic. antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
antiinfly; fungicide; antimutagen; cardiovascular; antianaemic; anaemia,
antiangregant; haemostatic; vulnerary; antiulcer; osteopathic; eccema;
dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 CATCTCACTTTCCTTGCTGGACAACACAGCCAAATCATCATCAACAAGTTCGTGAATAGCGT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      726 cogoatottoatocactocotggatytgaatgtoattoagoaggtoytogataatootoa 785
                     186 tcacgagggacttgagacagttgacaatactcttaaaygcatccttgagaaactgaaggt 245
                                                                                      361 CAAAGGCCTTAACCTGAGCTTCCCTGTCACGGGAATGTCACTGTGGCCGGGCCCATCAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                               421 TGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486 tggccagattatcaacctgaaagcctccttggacctcctgaccgcagtcacaattgaaac 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATCCCCAGACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 cateteaettteettgetggacaaacacagecaaateateaacaagttegtgaatagegt 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 gatcaacaegetgaaaageactgtateeteetgetgetgeagaaggagatatgteeaetgat 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 CCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                              241 AGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACTAACAGGGACATTTT 300
                                                                                                                                                                                                                                                 426 caaaggeettaacetgagetteeetgteacegegaatgteactgtggeegggeeeateat 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546 tgatccccagacaccagcctgttgccgtcctgggagaatgcgccagtgacccaaccag 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
Human protein encoding cDNA sequence SEQ ID NO:521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721 GCACAAAACCCAGCTGCAAACCCTCA 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               786 gcacaaaacccagctgcaaaccctca 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH99686 standard; cDNA; 1041 HP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH99686;
                                                                                                                                                                                                                                                   301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 cgacctaggagtgcttcagaaatccagtgcttggcaactggccaagcagaaggcccagga 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 tcacgagggacttgagacagttgacaatactcttaaaggcatccttgagaaactgaaggt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAGGCCCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 agctgagaaattgctgaacaatgtcatttctaagctgcttccaactaacacggacatttt 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGCGTGCTCACTGGGACCTCAGAGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1041 BP; 284 A; 299 C; 227 G; 231 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 579; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
                                                                                                                                                     23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                           22-DEC-2000; 2000WO-US35017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                         2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAM25745.
                              26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genemic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, enducrine or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparastic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to indentify specific (antipagonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 538 BP; 140 A; 126 C; 128 G; 124 T; 20 other;
                                             412 caaaqqccttaacctgagcttccctgtcaccgcgaatgtcactg 455
361 CAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 76; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to raise Ab, useful for diagnosis, to Identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence tay HSGSCl3R.
                                                                                                                                                                                                                                                                                                                            AAV44761 standard; DNA; 538 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WP1; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duan R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 - DEC - 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAV44761;
                                                                                                                                                                                                                                           RESULT
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Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; cancer; human; therapy; diagnosis; ss.

Expressed sequence tag HSGSC78R.

16-OCT-1998 (first entry)

AAV44764;

AAV44764 standard; DNA; 406 BP

AAV44764 RESULT

New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive

96US-0034429.

18-DEC-1997; 23-DEC-1996;

02-JUL-1998.

WO9828420-A1.

Homo sapiens.

(HUMA-) HUMAN GENOME SCI INC

WPI; 1998-377651/32.

Duan R,

and endocrine disorders and for drug screening

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This sequence represents an expressed sequence tag with homology to the
Disclosure; Page 77; 94pp; English.
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conditions associated with expressive here to conditions associated within the DNA of the invention. The DNA of the invention concates the human parotid secretory protein (HPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting) amplification or immune assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antipacterial, antipacterial, cantipacterial, antibacterial, cantipacterial or calls expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibacles (ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Calls containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 406 BP; 110 A; 95 C; 95 G; 100 T; 6 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 cagotttggaaacttgttctcctgtgcggcgtgctcactgggacctcagagtctcttctt 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CAGCTTTGGAAACTIGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCTTTTT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Score 218; DB 19; 100.0%; Pred. No. 3.2e-100;
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218; Conservative

Similarity

Query Match Best Local S

Matches

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Score 211; DB 19; Length 406; 28.38;

Query Match

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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention of the invention encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and panoreas which are associated with high levels of the protein is also useful as antifungal, antibacterial, or the protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                              71 AATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAAACCTGTTCTTCACGAGGGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                 131 CTTGAGAGAGTGAGAATACTCTTAAAGGCATCCTTGAGAAACTGAAGGTGGACGTAGGA 190
                                                                                                                                                                                                                                                                                                                                                      109 aatettggcaatgacetaagcaatglegtggataagetggaacetgltetteaegagga 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 cttgagacagttgacaatactctlaaaggcatccttgagaaactgaaygtcgacctagga 228
                                         0; Gaps
                                                                                                                    11 CTTTGGAAACTTGTTCTCTGTGCGGCGTGCTCACTGCGACCTCAGAGTCTCTTGTTGAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                     0; Indels
100.0%; Pred. No. 1.1e-96; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GIGCTICAGAATCCAGIGCTIGGCAACIGG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 gigoticagaaatccagigctiggcaactgg 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 78; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tag HSPMD56R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV44765 standard; DNA; 493 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; diagnosis; ss.
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-377651/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duan R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1996;
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                                             Matches
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to raise Ab, useful for diagnosis, therapy, for affinity purification and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures \cdot
                                                                                                                                                                                                                                             93 acacagecaaateateaacaayttegtyaalagegtgateaacaegetgaaaageaetgt 152
                                                                                                                                                                                                                                                                                                                         153 atcetecetyctgcagaaggagatatytecactgatecgcatettcatecactecetgga 212
                                                                                                                                                                                                                                                                                                                                                                    685 TGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCCT 744
                                                                                                                                                                                                                                                                                                                                                                                                         213 tytgaatgtcattcagcaggtcgtcgataatcctcagcacaaaacccagctgcaaaccct 272
                                                                                                                                                                                                   565 ACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGT 624
                                                                                                                                                                                                                                                                                  625 ATCCTCCTGCTGCAGAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTGGA 684
                                                                                                                                                            Gaps
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                                                                                                                       Length 493;
                                                                                                                                                            Indels
                                                          Sequence 493 BP; 118 A; 143 C; 107 G; 122 T; 3 other;
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                                                                                                                   24.4%; Score 182; DB 19; 100.0%; Pred. No. 5.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 27560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards J, Duclert A, Giordano J;
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                                                                                                                                100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping; ss.
                   to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC23485 standard; cDNA; 317 BP.
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                                                                                                                                                            Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-500381/45.
                                                                                                                                         Similarity
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                                                                                                                       Query Match
                                                                                                                                             Best Local
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identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hRSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention contained within the DNA of the invention. The DNA of the invention condess the human parotial secretory protein (hesp). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels or hPSP. The protein is also useful as antifungal, antibacterial, antipactasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parotid secretory protein; hPSP; digestive disorder; endocrine disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an expressed sequence tag with homology to the
        in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-immune defensive disorder; immune system disorder; cancer; human; therapy; diagnosis; ss
                                                                                                                                                                                    570 GCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCT 629
                                                                                                                                                                                                                                                 630 CCCTGCTGCAGGAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCTGGATGTGA 689
                                                                                                                                                                                                                                                                              61 ccctgctgcagaaygagatatgtccactgatccgcatcttcatccactccctggatgtga 120
                                                                                                                                                     Indels 0; Gaps
                                                                                                                                                                                                                  1 gocaaatcatcaacaagttcytgaatagcytgatcaacacgctgaaaagcactgtatcct 60
                                                                                                                                                                                                                                                                                                              690 ATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCCTCA 746
                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                      Length 317;
                                                                         Sequence 317 BP; 82 A; 100 C; 68 G; 67 T; 0 other;
                                                                                                                                                   0
                                                                                                                     23.7%; Score 177; DB 21; 100.0%; Pred. No. 1.9e-79; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 75-76; 94pp; English.
                                             expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tag HSGSA61R.
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                                                                                                                                                       Matches 177; Conservative
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                                                                                                                                         Local Similarity
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                                                                                                                          Query Match
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                                                                                                                                                                                           50 gatgettcagetttggaaacttgtteteetgtgeggegtgetcactgggaeetcagagte 109
                                                                                                                                                                                                                                                                           110 tettettgacaatettggcaatgacetaagcaatgtcgtggataagetggaacetgttet 169
                                                                                                                                                                                                                                    61 TCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120
                                                                                                             Gaps
                                                                                                                                                  1 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human digestive system antigen genomic sequence SEQ ID NO: 3374.
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0
                                                                Length 449;
                                                                                                             Indels
Sequence 449 BP; 122 A; 107 C; 106 G; 110 T; 4 other;
                                                                                                                                                                                                                                                                                                                         121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGG 159
                                                                21,3%; Score 159; DB 19; 100.0%; Pred. No. 2.4e-70;
                                                                                                                                                                                                                                                                                                                                                                    170 tcacqagggacttgagacagttgacaatactcttaaagg 208
                                                                                                           Mismatches
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2000US-0225266.
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14-AUG-2000; 2000US-0225267
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                                                                                                                  Conservative
                                                                                           Similarity
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17-MAR-2000;
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07-JUN-2000;
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07-JUL-2000;
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                                                                                             Local Simi
les 159;
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                                                                      Query Match
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2000US-0228924.
2000US-0229287.
2000US-0229343.
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2000US-0229345.
2000US-0229509.
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2000US-0246525.
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20-0CT-2000)
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20-0CT-2000)
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25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
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12-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
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14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
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20-0CT-2000;
20-0CT-2000;
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TCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GATGCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.3%; Score 159; DB 22; Length 7524; 100.0%; Pred. No. 2.4e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7524 BP; 2170 A; 1586 C; 1582 G; 2186 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                               2000US-0249208
2000US-0249209
2000US-0249210
2000US-0249211
2000US-0249212
2000US-0249213
2000US-0249213
2000US-0249214
2000US-0249216
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2000US-0250160.
2000US-0250391.
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2000US-0249218.
2000US-0249244.
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2000US-0249264.
2000US-0249265.
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                                                            2000US-0246611.
2000US-0246613.
2000US-0249207.
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2000US-0249299.
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2000US-0251990
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2000US-0246610.
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2000US-0246527
2000US-0246528
                        2000US-0246532
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Best Local Similarity 100.0
Matches 159; Conservative
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08-DEC-2000; 2
11-DEC-2000; 2
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17-NOV-2000;
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                                                                                                                       AAK08593;
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                                                                     AAK08593
                                                    RESULT
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                                                                                                                                                                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
   1037 tettettgacaalettggcaatgacetaagcaatgtegtggataagetggaaacetgttet 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 GGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACGCGCAGTCA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 gecceatcattggccagattatcaacctgaaagcetcettggacetcetgaecgcagtca 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe of the invention. Note: The sequence data for this patent did not form part of the \ensuremath{\mathsf{Note}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.6%; Score 154; DB 22; Length 581; 100.0%; Pred. No. 8.3e-68; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 8618; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #8618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 581 BP; 142 A; 161 C; 127 G; 151 T; 0 other;
                                                      121 TCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    531 ACCCAACCAGCATCTCACTTTCCTTGCTGGACAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                          ABA60313 standard; DNA; 581 BP.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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04-OCT-2000; 2000GB-0024263.
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Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      W0200157277-A2.
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                              ABA60313;
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                                                                                                                                           ABA60313
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 CAATTGAAACTGATCCCCAGACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTG 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                            Human brain expressed single exon probe SEQ ID NO: 8584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 acccaaccagcatctcactttccttgctggacaa 234
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   BP.
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2000US-0608408.
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03-AUG-2000, 2000US-0632366.
21-SEP-2000, 2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
AAK08593 standard; DNA; 581
                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                epilepsy; cancer; ss.
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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               Probe #8883 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 581;
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                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 581 BP; 142 A; 161 C; 127 G; 151 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%; Score 154; DB 22; 100.0%; Pred. No. 8.3e-68; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 ACCCAACCAGCATCTCACTTTCCTTGCTGGACAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 acccaaccagcatctcactttccttgctggacaa 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 8883; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK, Chen W,
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154; Conservative
                                                                  genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53.
                                                                                                                                  WO200157272-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2002
                                                                                                                                                                                                                                  04 - FEB - 2000;
                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA72852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 GGCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 gocceatcattggccagattatcaacctgaaagcctccttggacctcctgaccgcagtca 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 CAATIGAAACIGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAAIGGGCCAGTG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid
                                                                                                                                                 Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 9032; 658pp + Sequence Listing; English.
                                                                                                                  Human bone marrow expressed single exon probe SEQ 1D NO: 9032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.6%; Score 154; DB 22; Length 581; 100.0%; Pred. No. 8.3e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 581 BP; 142 A; 161 C; 127 G; 151 T; 0 other;
                                                                                                                                                                   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 ACCCAACCAGCATCTCACTTTCCTTGCTGGACAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 acccaaccagcatctcactttccttgctggacaa 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK, Chen W, Rank DR;
                 AAK34475 standard; DNA; 581 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001 (first entry)
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100. Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53
                                                                                                                                                                                                                                  WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI40197;
                                                  AAK34475;
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AAK34475
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Gaps

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WPI; 2001-483446/52.
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                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                04-OCT-2000;
                                                                               04-FEB-2000;
                                                                                                                     30-JUN-2000;
                                                                                                    26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local St.
153;
    09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                brains
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                    qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aattgaaactgateeccagacacaccagectgttgecgioetggagaatgggeaqtga 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412 GCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGAGTCAC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 AATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 geceateattggeeagattateaacetgaaageeteettggaeeteetgaeegeagteae 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.5%; Score 153; DB 22; Length 153; 100.0%; Pred. No. 2.7e-67; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ 1D NO 21157; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain expressed single exon probe SEQ ID NO: 21276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 153 BP; 38 A; 53 C; 30 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 cccaaccaqcatctcactttccttgctggacaa 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 CCCAACCAGCATCTCACTTTCCTTGCTGGACAA 564
                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
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                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                   2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                           03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
22-SEP-2000; 2000US-0235559.
04-OCT-2000; 2000GB-0024263.
                                                                             30-JAN-2001; 2001WO-US00669.
                                                                                                                   2000US-0180312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483447/52.
WO200157277-A2
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                                                                                                                   04-FEB-2000;
                                                                                                                                     26-MAY-2000;
                                                                                                                                                          30-JUN-2000;
                                       09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheiner's disease, multiple sciencis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aattgaaactgatccccagacacaccagcctgttgccgtcctgggagaatgcgccagtga 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 GCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACGGCAGTCAC 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 goccatcattggccagattatcaacctgaaagcctccttggacctcctgaccgcagtcac 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 21276; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 153 BP; 38 A; 53 C; 30 G; 32 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK47441 standard; DNA; 153 BP.
                                                                                                                200001S-0207456.
20000S-0608408.
20000S-0632366.
200001S-0234687.
20000S-0236359.
                                                                            2000US-0180312.
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30-JAN-2001; 2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #21962 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 GCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCAC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 AATTGAAACTGATCCCCAGACACACCCAGCCTGTTGCCGTCCTGGGAGAATGCGGCCAGTGA 531
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                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 21998; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 153 BP; 38 A; 53 C; 30 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        20.5%; Score 153; DB 22;
100.0%; Pred. No. 2.7e-67;
Live 0; Mismatches 0;
                                                                                                                                                                                                            analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 CCCAACCAGCATCTCACTTTCCTTGCTGGACAA 564
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                                                                                                                                    Hanzel DK, Chen W, Rank DR;
                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687.
2000US-0236359.
                           03-AUG-2000, 2000US-0632366.
21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                               the probes of the invention.
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2000US-0207456.
2000US-0608408.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                        04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder; ss.
                                                                                                                                                                 WPI; 2001-488900/53
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                     Penn SG,
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 GCCCATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCAC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 AATTGAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGA 531
                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     1 goccatcattggccagattatcaacctgaaagcctccttggacctcctgaccgcagtcac 60
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                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                              20.5%; Score 153; DB 22; Length 153; 100.0%; Pred. No. 2.7e-67; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Sequence 153 BP; 38 A; 53 C; 30 G; 32 T; 0 other;
                                                                                                                           analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 CCCAACCAGCATCTCACTTTCCTTGCTGGACAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ 1D No 21962; 654pp; English.
                                             Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 77; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed sequence tag HSPAll4R.
                (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                           Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; diagnosis; ss.
                                                                            WPI; 2001-488897/53.
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                                             Penn SG,
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This sequence represents an expressed sequence tag with homology to the DNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding permonic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the sally ary gland, thymus and panceas which are associated with high levels of hPSP. The protein is also useful as antifungal, antipacterial,
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                                                                                                                                                                                                                                                           antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (anti)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 GCGTGATCAACACGCTGAAAAGCACTGTATCCTCCTGCTGCTGCAGAAGGAGATATGTCCAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 TGATCCCCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAATC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 tgatccgcatcttcatccactcctygatgtgaatgtcattcagcaggtcgtcgataatc 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 gcgtgatcaacacgctgaaaagcactgtatcctcctgctgcagaaggagatatgtccac 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%; Score 150; DB 19; Length 374; 100.0%; Pred. No. 8.8e-66; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 374 BP; 86 A; 123 C; 82 G; 78 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 CICAGCACAAACCCAGCIGCAAACCCTCA 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 ctcagcacaaaacccagctgcaaaccctca 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed sequence tag HSGSAB9R
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UNA of the invention, and is all so specifically stated as not being contained within the DNA of the invention. The DNA of the invention of the invention of the invention. The DNA of the invention concained within the DNA of the invention. The DNA of the invention concades the human parotid secretory protein (heBs). The hBsP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hBsP (in standard blotting) amplification or immune assays), particularly corresponding application is diagnosis of cancers of the system disorders. A particular application is diagnosis of cancers of the system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and panoreas which are associated with high levels of hFsP. The protein is also useful as antifungal, antibacterial, antibacterial, antibacterial, antibacterial cand antiviral agents and may be expressed in streaming the protein or calls expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPsP production. Cells containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parotid secretory protein; DPSP; digestive disorder; endocrine disorder;
                                                                                           This sequence represents an expressed sequence tag with homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 gatgetteagetttggaaaettgtteteetgtgegggggtgeteaetgggaeeteagagte 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-immune defensive disorder; immune system disorder; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAIGCTICAGCTITGGAAACTIGITCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 359 BP; 94 A; 79 C; 90 G; 90 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%; Score 110; DB 19;
100.0%; Pred. No. 1.6e-45;
and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                             Disclosure; Page 76-77; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to identify hPSP-binding proteins.
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Best Local Similarity 100.0%; Pr
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This sequence represents a PCR primer for DNA encoding the human parotid secretory protein (HBSP) of the invention. The HPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (antipagonists, eg antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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and endocrine disorders and for drug screening
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                                                                                                                        Example 1; Page 54; 94pp; English.
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Matches 28; Conservative
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\begin{array}{c} \mathsf{F} \times \mathsf{G} \times \mathsf{G} \\ \mathsf{
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chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encodes the human parotid secretory protein (hPSP). The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an expressed sequence tag with homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. digestive
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                                                                                                                                                                                                                                                                                                                                                                                                                               3.4%; Score 25; DB 19; Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0.018;
has 0; Indels
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                                                                                                                                                                                                                                                                                                                                                             Sequence 43 BP; 8 A; 13 C; 9 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ....
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                   to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATGCTTCAGCTTTGGAAACTTGTTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 atgetteagetttggaaaettgtte 43
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Matches 25; Conservative
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salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to identify hPSP-binding proteins.
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Sequence 395 BP; 110 A; 116 C; 83 G; 70 T; 16 other;

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                           0; Gaps
3.2%; Score 24; DB 19; Length 395;
      0.057;
0,057;
0; Indels
            Pred. No. 0.0
Mismatches
                                                      670 CATCCACTCCCTGGATGTGAATGT 693
3.2%;
100.0%; Pre
                                                                                   60 catecactecetyyatgtgaatgt 83
                                                                                                                                                       AAV44770 standard; DNA; 36 BP
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                             Conservative
               Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                     AAV44770;
   Query Match
                             Matches
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Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human; PCR primer for human parotid secretory protein coding sequence. therapy; diagnosis; PCR primer; ss.

W09828420-A1. Homo sapiens. 02-JUL-1998 Synthetic

97WO-US23522. 96US-0034429. 18-DEC-1997; 23-DEC-1996; (HUMA-) HUMAN GENOME SCI INC

Duan R, Ruben SM;

WPI; 1998-377651/32.

New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening

Example 1; Page 54; 94pp; English.

This sequence represents a PCR primer for DNA encoding the human parotid secretory protein (hPSP) of the invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting, amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hPSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral agents and may be expressed in vivo from the DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (AD), polypeptides and antisense nucleic acids, which are potentially useful for treating 

the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length course. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by

sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

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conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                             Gaps
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                                                                                                   2.9%; Score 22; DB 19; Length 36; 100.0%; Pred. No. 0.59; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID 18545; 2537pp + CD ROM; English.
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T, Wakamatsu A, Nagai K,
                                                                Sequence 36 BP; 6 A; 7 C; 12 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:18545.
                                                                                                     2.5%;
100.0%; Pit
0;
                                                                                                                                                                                                                                           AAH18450 standard; cDNA; 1730 BP
                                                                                                                                                       725 AAAACCCAGCTGCAAACCCTCA 746
                                                                                                                                                                               36 AAAACCCAGCTGCAAACCCTCA 15
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                              Conservative
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                                                                                                                  Local Similarity es 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             full-length cDNAs
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                                                                                                                                                                                                                                                                      AAH18450;
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                                                                                                        Query Match
                                                                                                                                                                                                                     RESULT 27
                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA. The protein, or cells expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive PESP production. Cells containing the DNA are used to express the recombinant protein and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and
the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3632 represent human amino aequences; and AAH13629 to AAH3632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                      2.8%; Score 21; DB 22; Length 1730; 100.0%; Pred, No. 1.9; of indels of mismatches
                                                                                                                                                          Sequence 1730 BP; 547 A; 358 C; 383 G; 442 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                             1113 TGAGAAATTGCTGAACAATGT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV44768 standard; DNA; 360 BP.
                                                                                                                                                                                                                                                                                                                244 TGAGAAATTGCTGAACAATGT 264
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                                                                                                                  of the present invention.
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
       8×00000×8
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AMW23945) of pig G-protein required phosphatidylinositol-3 klnase, a heterodimeric enzyme which produces the intracellular messenger phosphatidylinositol (3.4.5)-triphosphate in response to activation of trimeric G protein-linked receptors. This novel protein, which also contains a catalytic subunit, pl20 (see AAV04634), is found in cells of haemacopoletic origin and is involved in immune system responses which cause inflammation. The pl01 subunit is largely presence of activated trimeric C proteins. pl01 cDNA was obtained from a pig neutrophil cDNA library using a degenerate oligonucleotide probe (see AAAT99714) based on an isolated pl01 tryptic peptide. The pl01 cDNA clone in pCMV3mycpl01 is deposited as ATCC 97636. The
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase, p101 and p120 subunits - useful for diagnosis, drug screening, clinical trial monitoring and treatment of inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-beta-gamma regulated phosphatidylinositol-3' kinase; pig; phosphoinositide 30H kinase; Pi3K; signal transduction; phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor; transgenic animal; knockout animal; inflammation; arthritis; septic shock; adult respiratory distress syndrome; pneumonia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma, allergy, reperfusion injury, atherosclerosis, cancer;
Alzheimer's disease; cancer; antisense, ribozyme; diagnosis;
                                                                                     Query Match 2.7%; Score 20; DB 19; Length 360; Best Local Similarity 100.0\%; Pred. No. 6.1; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine phosphoinositide 30H-kinase p101 subunit cDNA.
                                  Sequence 360 BP; 99 A; 91 C; 83 G; 60 T; 27 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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to identify hPSP-binding proteins.
                                                                                                                                                                                                                                                                                                       AAV04633 standard; cDNA; 4692 BP.
                                                                                                                                                                      429 TTATCAACCTGAAAGCCTCC 448
                                                                                                                                                                                           30 ttatcaacctyaaagcctcc 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; drug screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                             AAV04633;
                                                                                                                                                                                                                                                                                    AAV04633
                                                                                                                                                                                                                                                                                                                                             Sox
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invention encompasses pig and human p101 and p120 nucleotides, host cell expression systems, p101 and p120 proteins (see Awa23946-49), fusion proteins, polypeptides and peptides, antibodies to these proteins, and transpent animals and knockout animals. Compounds which are useful for treating inflammatory response disorders can be identified by screening inflammatory response and storders can be identified by screening inflammatory response and insorders can be identified by screening inflammatory response cutivated p13K, or a cultured host cell that expresses the p101 aprol specially by disrupting the interaction between the p101 and p120 subunits can be used to treat arthritis, septic shock, adult respiratory distress syndrome (ARDS), pneumonia, softwa, allergies, reperfusion injury, atherosclerosis, cancer and althermer's disease. Signalling-incompetent p101 (preferably a deletion mutant) oligonucleotide constructs, antiseise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphoinositide 3-hydroxykinase; P13K; trimeric G protein; porcine; adapter subunit; regulatory subunit; p101; p120; catalytic subunit; detection; diagnosis; activation disorder; haematopoietic system; treatment; immune disorder; inflammation; arthritis; septic shock; adult respiratory distress syudrome; pneumonia; asthma: allergy, reperfusion injury; atherosclerosis; Alzheimer's disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding regulatory (p101) and catalytic (p120) subunits of a heterodimeric phosphatidylinositol-3' kinase - useful in treatment and diagnosis of immune system disorders, e.g. arthritis, cancer and Alzheimer's disease
                                                                                                                                                                                                                                                                                                           oligonucleotides, triple helix forming eligenucleotides, ribozymes or recombinant DNA constructs that act through targeted homologous recombination are all useful for inhibiting expression of the plo1 subunit, especially by delivery to cells of haematopoietic origin.

(All claimed). The nucleic acids and their products can also be used for diagnosis, drug screening and clinical trial monitoring of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 20; DB 19; Length 4692; 100.0%; Pred. No. 6.1; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porcine G-protein regulated PI3K pl01 adapter subunit DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4692 BP; 916 A; 1559 C; 1394 G; 823 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hawkins PT, Stephens L;
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96US-0672211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory diseases.
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Best Local Similarity
Matches 20; Conservē
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27-JUN-1996;
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This sequence encodes a novel adapter subunit, pl01, (also known as the regulatory subunit) from porcine phosphoinositide 3-hydroxykinase (PISK) which is regulated by beta agamma subunits of trimmeric G-protein. Nucleic acid coding for pl01 or pl20, or their fragments, are used as probes and primers for identifying pl01 or pl20 gene mutations, allelic variations or regulatory defects, particularly for the diagnosis of activation disorders for susceptibility) in cells of the hematopoletic system. The related proteins, antibodies, agonists and antagonists can be used to treat or screen for potential agents for treating immune disorders, particularly inflammation, e.g. arthitis, septic shock, adult respiratory distress syndrome, pneumonia, asthma, allergies, reperfusion injury, atherosclerosis, Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p101 protein; p120 protein; regulatory subunit; immune system disorder; trimeric G-protein regulated P13k; phosphoinositide 30H kinase; asthma; inflammatory response disorder; arthritis; septic shock; allergy; adult respiratory distress; cancer; reperfusion injury; atheroscienosis; Alzheimer's disease; haematopoietic lineage cell activation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated pl01 regulatory polypeptide, a subunit of the trimeric G-protein regulated PI3K, is useful for screening compounds which can be used to treat inflammatory response disorders
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The invention relates to the human pl01 regulatory protein,
                                                                                                                                                                                                                                                                                                                                    Sequence 4692 BP; 916 A; 1559 C; 1394 G; 823 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pig pl01 regulatory subunit coding sequence.
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              Example IX; Fig 1A-D; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2000 (first entry)
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02-OCT-2000;
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               which is a subunit of the trimeric G-protein regulated phosphoinositide
assays to detect compounds which can be used in screening
response disorders. The compounds which can be used to reat inflammatory
response disorders. The compounds identified may be antagonists or
agonists of G protein-regulated P13% gene expression and/or p101 or p120
gene product activity. These compounds may then be used to control immune
system disorders, in particular arthritis, septic shock, adult
respitatory distress, asthma, allergies, reperfusion injury,
respitatory distress, asthma, allergies, reperfusion injury,
ceptides can be used in the detection of mutant or inappropriately
expressed p101 regulatory subunits for the diagnosis of immune disorders
assist in devising a proper treatment or therapeutic regime. Using
genetically engineered host cells to screen for compounds also allows
compounds which affect the signal transduced by the activated p101
regulatory subunit to be identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antilosor; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nervous system related polynucleotide SEQ ID NO 60.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4692 BP; 916 A; 1559 C; 1394 G; 823 T; 0 other;
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07-JUL-2000; 2000US-0216647.
07-JUL-2000; 2000US-0216880.
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02-MAR-2000; 2
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07-JUN-2000; 2
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26-JUL-2000;
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                                                                                                                                        Query Match
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2000US-0249216.
2000US-0249217.
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antihifiammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialaepetic; antiolocer; anticonvulsant; antifungal; antiparasitic; cardianctic; antiolocer; anticonvulsant; antifungal; antiparasitic; cardianctis; immune disorder; cardiavascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0235834.
2000US-0235836.
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The first transfer of 
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20000S-0249244.
20000S-0249265.
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20000S-0249297.
20000S-0249299.
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17 - NOV - 2000;
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Gaps

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Query Match 2.5%; Score 19; DB 22; Length 451; Best Local Similarity 100.0%; Pred. No. 20; Matches 19; Conservative 0; Mismatches 0; Indels

367 CCTTAACCTGAGCTTCCCT 385

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2000US-0241809.
2000US-0241826.
2000US-0241826.
2000US-0244617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human nervous system related polynucleotide SEQ ID NO 6779
                                                                                                                                                                                                                                  ABA14448 standard; DNA; 766 BP
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AAS91657/
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                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB1467B-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, reatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.
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Best Local Similarity 100.(
Matches 19; Conservative
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The present sequence encodes the human granulocytic ehrlichiosis (HGE) isolate NCH-1 eM4 protein. The present invention describes HGE DNA molecules and proteins, and methods which can be used for the detection, treatment and prevention of HGE and related disorders caused by infection by protein and DNA molecules which encode them, from the agent of HGE (aoHGE). An antibody which binds to an HGE protein can
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Human; granulocytic ehrlichiosis; HGE; aoHGE; diagnosis; vaccine;
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100.0%; Pred. No. 20;
Live 0; Mismatches
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                                                                                                                                                      Location/Qualifiers
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Matches 19; Conservative
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                                     detection; infection; ss.
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2000US-0180628
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08-SEP-2000
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             24-FEB-2000;
02-MAR-2000;
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    polypeptide (II) sequences to isolated polymuricalize (I) and propertide (II) sequences to isolated polymuricalization probes, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The collamostics as expressed sequence tags of universal production of (II). The collamostic sequence tags of the restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) and tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Asset197 Asset364 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40806
                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 19; DB 23; Length 3636; 100.0%; Pred. No. 20; trive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                         Claim 1; SEQ ID No 27461; 103pp; English.
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                                                              Tang YT;
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31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                              Drmanac RT, Liu C,
                                                                                      WPI; 2001-639362/73.
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                                      (HYSE-) HYSEQ INC.
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2000US-0231414.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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2000US-0249216.
2000US-0249217.
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2000US-0251869.
2000US-0251989.
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2000US-0249265.
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2000US-0244617.
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                                                        20-OCT-2000;
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17-NOV-2000;
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AAX54951 to AAX64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAX64703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAX64942 to AAX64500 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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Disclosure; SEQ ID NO 40806; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59060 BP; 14758 A; 13705 C; 13620 G; 16977 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 19; DB 22; Length 59060; 100.0%; Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL17739 standard; DNA; 846 BP
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Matches 19; Conservative
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                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wall D, Trawick JD, Carr GJ;
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                            2.4%; Score 18; DB 23; Length 846;
100.0%; Pred. No. 63;
.ive 0; Mismatches 0; Indels
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                                                                                                                         Sequence 846 BP; 196 A; 215 C; 241 G; 194 T; 0 other;
                                                                                         at itp.wipo.int/pub/published_pct_sequences.
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26-MAY-2000; 2000US-207737P.
27-NOV-2000; 2000US-242578P.
27-NOV-2000; 2000US-257825P.
22-DEC-2000; 2000US-257931P.
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Best Local Similarity 100.0
Warshes 18; Conservative
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for homologous nucleic acids which are required for cell proliferation in
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antiinflammatory; haemostatic; malignant tumour; haemopathy;
HIV infection; immunological disease; inflammation; ss.
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              a wide variety of organisms. The present sequence encodes an essential protaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                           Ouery Match 2.4%; Score 18; DB 23; Length 1173; Best Local Similarity 100.0%; Pred. No. 63; Matches 18; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 63; Length 1274;
Matches 18; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                        Sequence 1173 BP; 362 A; 205 C; 281 G; 325 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunological diseases and various inflammations
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                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PDZ protein 20 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                      AAH73917 standard; cDNA; 1274 BP.
                                                                                                                                                                                                                                                                                 893 gayaaattgctgaacaat 910
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
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Watanabe CK, Wood WI, Zhang 2:
                                                                                                                                                                                           Human DNA encoding PRO polypeptide sequence #304.
                                              AAS46228 standard; cDNA; 2265 BP.
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2000US-194449P.
2000US-194647P.
2000US-195975P.
2000US-196000P.
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2000US-196690P.
2000US-196820P.
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2000US-189328P.
2000WO-US06884.
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2000US-192655P.
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05-JUN-2000; 2000MO-USIS2628-JUL-2000; 2000MO-US20710.
28-JUL-2000; 2000MO-US2710.
22-AUG-2000; 2000MO-US23328.
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2000US-191048P.
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2000US-199397P.
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2000US-186968P
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2000WO-US30952.
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20-DEC-2000; 2000WO-US34956.
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11-APR-2000; 2
11-APR-2000; 2
11-APR-2000; 2
11-APR-2000; 2
18-APR-2000; 2
25-APR-2000; 2
25-APR-2000; 2
25-APR-2000; 2
35-APR-2000; 2
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22-MAY-2000; 2
30-MAY-2000; 2
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21-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                             PCR primer.
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RESULT 41
                       AAS46228/c
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primers for PRO polypeptides of the invention. The sequences of the primers for PRO polypeptides of the invention. The sequences of the primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a control sample indicates the presence of a tumour in the mammal. Mammals include dogs, catts, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adereal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PIGR-1; immunoglobulin; rheumatoid arthritis; psoriasis; multiple sclerosis; systemic lupus erythematosus; diagnosis; receptor; infilammatory bowel disease; ss.
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                                                                           Claim 2; Fig 607; 774pp; English.
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Matches 18; Conservative
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The present sequence encodes a new receptor polypeptide designated piges. Which is a member of the immunoquobulin (19) superfamily. PIGR-1 proteins and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the PIGR-1 gene, and can diagnose consists and antaqonists PIGR-1 protein imbalance by determining PIGR-1 protein imbalance by determining PIGR-1 protein can be used to screen for agonists and antaqonists PIGR-1 protein imbalance by determining PIGR-1 consists and antaqonists PIGR-1 protein for activate (agonist) or inhibit (antagonist) PIGR-1 activity, in addition to direct administration of antisense sequences to prevent expression, or PIGR-1 polynucleotides to treat conditions associated with a lack of PIGR-1 protein Gene therapy may also be used to affect endogenous PIGR-1 protein continuous and prevent disease, and for isolating PIGR-1 protein expression. PIGR-1 antibodies are useful for inducing an immune response to immunise and prevent disease, and for isolating PIGR-1 proteins can be administered directly or as a vaccine to incoulate procession and prevented and treated include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis, multiple sclerosis, psoriasis, systemic lupus erythematosus and inflammatory bowel disease. The PICR-1 protein is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.
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100.0%; Pred. No. 63;
Live 0; Mismatches 0; Indels
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ID ABL17740 standard; DNA; 2643
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18; Conservative
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Best Local S
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is expressed specifically upon re-oxygenation of astrocytes after exposure to low-oxygen conditions. The protein is involved in brain ischaemia, so it and the related gene are useful for elucidation of the mechanism of ischaemia. They are also useful for the creation of a model animal with diseases accompanying ischaemia or for development of drugs for prevention or treatment of such diseases. Antibodies to the protein are useful for determining the severity of diseases caused by ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat; YT521 gene; re-oxygenation; astrocyte; low-oxygen condition; brain; ischaemia; animal model; drug screening; ds.
                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brain ischaemia-related gene and protein - useful for elucidation of mechanisms of ischaemia and in animal models for screening drugs for prevention or treatment of ischaemia
                                                                                                                                                                                                                                                            Gaps
cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                   2.4%; Score 18; DB 23; Length 2643; 100.0%; Pred. No. 63; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                   Sequence 2643 BP; 756 A; 531 C; 561 G; 795 T; 0 other;
                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAT91872 standard; cDNA to mRNA; 3224 BP.
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317.2455
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                                                                                                                                                                                                                       2.4%;
100.0%; Pro-
                                                                                                                                                                                                                                                                                                                                  2598 ACCGCAGTCACAATTGAA 2581
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                                                                                                                                                                                                                                                                                             461 ACCGCAGTCACAATTGAA 478
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                           (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW30749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat YT521 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus
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2.4%; Score 18; DB 18; Length 3224;

Query Match

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WO200171042-A2.
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                                          26-MAR-2002
                                                                                                                                                                                                                      27-SEP-2001.
          ABL18573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                         Gaps
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                                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 22088.
                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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100.0%; Pred. No. 63;
iive 0; Mismatches 0; Indels (
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                        0; Indels
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100.0%; Prec. ...
0; Mismatches
        Pred. No. 63;
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ID ABL09202 standard: cDNA; 3839 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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                                                     660 TCCGCATCTTCATCCACT 677
                                                                                    1002 TCCGCATCTTCATCCACT 985
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                                                                                                                                                                                                                                 (first entry)
     Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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ABL18573
ID ABL1XX
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 30935.
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                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 7192.
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100.0%; Pred. No. 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li PWD,
                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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(first entry)
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                                                                                                                                      pharmaceutical; gene; ds.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                   Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75
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Nagai K, Otsuki T;

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Sugiyama T, Wakamatsu A,
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  Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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  capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                (ABB57737 ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
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                                                                                                                                                                                      Claim 1; SEQ ID NO 30935; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                    Sequence 4360 BP; 1145 A; 1067 C; 1110 G; 1038 T; 0 other;
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                                                                                             Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:18880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                4009 geceateattggecayat 4026
                    23-MAR-2001; 2001WO-US09231.
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                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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2000JP-0118776.
2000JP-0183767.
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hes 18; Conservative
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                                                                                             Venter JC, Adams M,
                                                                                                                WPI; 2001-656860/75
                                                                       (PEKE ) PE CORP NY.
                                                                                                                            P-PSDB; ABB68048
                                                                                                                                                                    interactions -
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 27-SEP-2001
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antiseense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13621 to AAH13629 and AAH13631 to AAH13642 represent human cDNA sequences, and AAH13632 to AAH13632 represent human amino acid sequences, and AAH13632 to AAH13632 represent human amino acid sequences, and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDMAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 18880; 2537pp + CD ROM; English.
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11-JUL-2000; 2000US-0614150.
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WPI; 2001-318749/34.
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cell-cell interactions in higher eukaryotes for the development of
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                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                     Claim 1; SEQ ID NO 4687; 21pp + Sequence Listing: English.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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100.0%; Pred. No. 63;
Live 0; Mismatches 0; Indels
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   Score 18; DB 23; Length 6846; Pred. No. 63;
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Pred. No. 63;
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Live 0; Mismatches
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11-JUL-2000; 2000US-0614150.
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(ABB57737-ABB72072).
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ABL18572/C
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Human; endocrine antigen; ds; cytostatic; antiinfertility; antidiabetic;
                                                            thyroid-active; adrenal-active; androgenic; gastric; gene therapy; antibody; endocrine disorder; hormone imbalance; reproductive disorder: endocrine cancer; pancreatic disorder; diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder; hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.
                                   Human genomic DNA for novel endocrine antigen, SEQ ID No 814.
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2000US-0180628.
2000US-0184664.
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2000US-0231243
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                  17-DEC-2001 (first entry)
                                                                                                                                       W0200155319-A2
                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                16-MAR-2000;
17-MAR-2000;
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01-SEP-2000;
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07-JUL-2000;
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14-AUG-2000;
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08-NOV-2000; 20000S-0246475.

08-NOV-2000; 20000S-0246476.

08-NOV-2000; 20000S-0246477.

08-NOV-2000; 20000S-0246523.

08-NOV-2000; 20000S-0246524.

08-NOV-2000; 20000S-0246524.

08-NOV-2000; 20000S-0246526.

08-NOV-2000; 20000S-0246527.

08-NOV-2000; 20000S-0246527.

08-NOV-2000; 20000S-02466528.

08-NOV-2000; 2000US-0246610.

08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0246611.

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08-NOV-2000; 2000US-0246611.
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2000US-0237037.
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2000US-0241808.
2000US-0241808.
2000US-0241826.
2000US-024617.
2000US-0246475.
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20000S-0249208.
20000S-0249210.
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2000US-0249264.
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2000US-0249218.
2000US-0232398.
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21-SEP-2000; 2
21-SEP-2000; 2
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27-SEP-2000; 2
29-SEP-2000; 2
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01-NOV-2000; 2
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29-SEP-2000;
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26-SEP-2000;
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The invention relates to CDNAs encoding novel human endocrine antigens or a fragment having biological activity, a domain, an epitope, full length procein, variant, allelic variant or a species homologue of the CDNA/antigen. The DNAs and polypeptides are useful for preventing, creating or ameliorating a medical condition when administered e.g. by gene therapy or antisense-therapy). Identifying mutations in the genes coding for the antigens is useful for diagnosing a pathological condition or a susceptibility to a pathological condition. The DNAs, antigens and antibodies raised against the antigens useful for treating, preventing and/or prognosing disorders related to the endocrine system or hormone imbalance or reproductive disorders, cancers of endocrine tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands (e.g. hisutism), overies, the thyroid (e.g. hypothalamus and testes (e.g. vanishing testes syndrome), many examples of the pare of given in the specification. The present
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                                                                                                    06-DEC-2000; 2000US-0251479;
08-DEC-2000; 2000US-0251856;
08-DEC-2000; 2000US-0251868.
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11-DEC-2000, 2000US-0254097.
05-JAN-2001, 2001US-0259678.
   2000US-0251030.
2000US-0251988.
                                                                         2000US-0256719
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05-DEC-2000;
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2000US - 0236376
2000US - 0236376
2000US - 0236376
2000US - 0237637
2000US - 0237652
2000US - 023762
2000US - 023
                           2000US-0235484.
2000US-0235834.
2000US-0235836.
2000US-0235353.
diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder; hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.
                                                                                                                                              31-Jan-2000; 2000US-0179065.

24-FEB-2000; 2000US-0180628.

25-MAR-2000; 2000US-01806361.

16-MAR-2000; 2000US-01806374.

17-MAR-2000; 2000US-0199123.

19-MAY-2000; 2000US-0199123.

19-MAY-2000; 2000US-0199123.

19-MAY-2000; 2000US-0205515.

10-JUL-2000; 2000US-0205515.

11-JUL-2000; 2000US-0217486.

11-JUL-2000; 2000US-0217486.

11-JUL-2000; 2000US-0217486.

11-JUL-2000; 2000US-0217486.

11-JUL-2000; 2000US-022056.

11-JUL-2000; 2000US-0220575.

11-JUL-2000; 2000US-0220575.

11-JUL-2000; 2000US-0220575.

11-JUL-2000; 2000US-0220575.

11-JUL-2000; 2000US-022556.

11-JUL-2000; 2000US-022576.

11-JUL-2000; 2000US-022576.

11-JUL-2000; 2000US-022576.

11-JUL-2000; 2000US-022934.

11-JUL-2000; 2000US-022934.

11-ZEP-2000; 2000US-022934.

11-ZEP-2000; 2000US-022939.

11-ZEP-2000; 2000US-023239.

11-ZEP-2000; 2000US-023339.

11-ZEP-2000; 2000US-023339
                                                                                                                         17-JAN-2001; 2001WO-US01335
                                                                    WO200155319-A2.
                                             Homo sapiens
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Myers EW;

Li PWD,

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Venter JC, Adams M,
        (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                      tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the hypothalamus and testes (e.g. vanishing testes syndrome), many examples of diseases and disorders are given in the specification. The present sequence is genomic DNA fragment form a gene encoding an endocrine
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                                                                                                                                                                                           The invention relates to cDNAs encoding novel human endocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%; Score 18; DB 22; Length 8116;
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live 0; Mismatches
                                                                                                                                                                   Disclosure; SEQ ID No 815; 558pp; English.
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                                                     Ruben SM;
                          (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678
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                                                   Rosen CA, Barash SC,
                                                                           WPI; 2001-457726/49.
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ABL08532/C
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell:cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                 genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic library: bacteria; human upper airway; otitis media; sinusitis;
                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
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100.0%; Pred. No. 63;
                                                                                                                                                                                                         Claim 1; SEQ 1D NO 20078; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8844 BP; 2046 A; 2085 C; 2096 G; 2617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bronchopulmonary; endocarditis; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berg KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF28549 standard; DNA; 92407 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7058 CCAACCAGCATCTCACTT 7041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 CCAACCAGCATCTCACTT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-2000; 2000WO-US16649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic fragment #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072).
WPI; 2001-656860/75
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nes 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-041427/05.
                                  P-PSDB; ABB64429
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see ARZE8544, ARZE8544). The library has a number of uses described in the specification e.g. is useful for aldentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray: The probes are useful for verlifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring yene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                              Sequence 92407 BP; 26788 A; 17581 C; 20150 G; 27888 T; 0 other;
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                     2.4%; Score 18; DB 22; Length 92407;
100.0%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 10244; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human breast cell single exon nucleic acid probe #10244.
                                                                                                                                                                                                                                                                                 100.0%; Pred no included of Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA51549 standard; DNA; 249 BP
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2000US-0234687.
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                569 AGCCAAATCATCAACAAG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease; cancer; ss.
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                               and meningitis.
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart with a microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, e.g. cardiovascular diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
                  greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                  than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far great diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #14986 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                            Score 17; DB 22; Length 249; Pred. No. 2e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                         Sequence 249 BP; 46 A; 76 C; 54 C; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID No 14986; 530pp; English.
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                                                                                                                                                                                                                                                2.35,
100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA36520 standard; DNA; 249 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-ADG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02343687.
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04-0CT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                          332 GATGTCAAAGCTGAACC 348
                                                                                                                                                                                                                                                                                                                                                               170 GATGTCAAAGCTGAACC 154
                                                                                                                                                                                                                                                                                      17; Conservative
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                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                       RESULT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant: transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocloi; homeodomain; homeoci; homeodomain; homeoci; LIM domain; AP2; ERBBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
  specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                         Gaps
                                                                                                                                                       .,
                                                                                                                  2.3%; Score 17; DB 22; Length 249; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis transcription factor DNA sequence #321.
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                                                        Sequence 249 BP; 46 A; 76 C; 54 G; 73 T; 0 other;
                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGrath A, Shenk MA, Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FLET-) FLETCHER CHALLENGE FORESTS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 129; 747pp; English.
                                                                                                                                                                                                                                                                                                                                    AAC56190 standard; DNA; 350 BP.
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                                                                                                                                                                                                 332 GATGTCAAAGCTGAACC 348
                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001 (first entry)
                                                                                                                                                                                                                                    170 GATGTCAAAGCTGAACC 154
                                                                                                                                                           17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eucalyptus grandis.
                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1999;
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                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                     AAC56190
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2.3%; Score 17; DB 21; Length 350;

Query Match

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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokime, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human: cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                    Gaps
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Pred. No. 2e+02; 0; 1ndels
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Mismatches 0;
                100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 574.
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                                                                                                                                                                                                                                                                                                                                       AAI80514 standard; cDNA; 395 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001 (first entry)
                                                                                                                                                                                  244 cogcatcttcatccact 260
                                                                                                                      661 CCGCATCTTCATCCACT 677
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                                                                                                                                                                                                                                                                                                                                                                                                         AAI80514;
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ABA26652 standard; DNA; 454 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genemic DNA predicted to detecting a prodisposition and/or gene discovery, and for detectining predisposition and/or prognosing breast General detections and prodisposition and/or prognosing breast General detections.
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                                                                                                                                                                                                                                          Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ 1D NO 5144; 327pp + sequence listing; English.
                                                                                                                                                                                       Human breast cell single exon nucleic acid probe #5144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK, Chen W, Rank DR;
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                                  ABA46449 standard; DNA; 454 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN 2000; 20000S-0608408.
31-JUN 2000; 2000US-052366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02368759.
04-OCT-2000; 2000GB-00242633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456.
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                                                                                                                                         01-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                             disease; cancer; ss.
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                                                                                        ABA46449;
     ABA46449/C
ID ABA46
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microbarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes for
                                                      Probe #5118 for gene expression analysis in human heart cell sample.
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                                                                                                                       Human, gene expressión; heart, microarray; vascular system; probe,
cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 5118; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                        congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0207456.
2000US-0608408.
2000US-0632366.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
24-0CT-2000; 2000GB-0024263.
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23-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                      WO200157274-A2.
                                                                                                                                                                                                                                                            Homo sapiens.
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Score 17; DB 22; Length 454; Pred. No. 2e+02; 0; Mismatches 0; Indels

Best Local Similarity 100.0%; Pred. No. 2e+(Matches 17; Conservative 0; Mismatches

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Query Match

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(MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000;
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                                                                                                           Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a novel Arthropod defensin from S. canidens DS clone ascl.px03. The invention retates to novel polymoclectides encoding Arthropod defensin polypeptides. The polypeptides and polymuclectides of the invention have antimicrobial activity. The polynuclectides may be used to genetically engineer cells and organisms, especially plants, to alter their resistance to a wide range of microbial pathogens. The polynuclectides may also have a use in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
         Arthropod defensin cDNA from Scolopendra canidens DS clone ascl.pk03.
                             Arthropod; defensin; ascl.pk03; antimicrobial; microbial pathogen;
                                                                                                                                                                                                                                                                                New polynucleotides encoding Arthropod defensin polypeptides for improving the microbial resistance of plants and animals by gene
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100.0%; Pred. No. 2e+02;
Live 0; Mismatches 0; Indels
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                                                                                                         /product= "Defensin"
                                                                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        Claim 6; Page 17; 22pp; English.
                                                                                                                                                                                                                              Presnail JK, Weng Z, Wong JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA63465 standard; DNA; 570 BP
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                                                                                                                                                                     12-APR-2001; 2001EP-0303488
                                                                                                                                                                                         14-APR-2000; 2000US-197279P
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                                                           Scolopendra canidens DS.
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nes 17; Conserva
                                        qene therapy; ss
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #9129 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression; heart; microarray; vascular system; probė; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 11770; 639pp + sequence listing; English.
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100.0%; Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congenital heart disease; ss.
                                                30-JUN-2000; 2000US-060B40B.
03-AUG-2000; 2000US-0632866.
21-SEP-2000; 2000US-02346B7.
27-SEP-2000; 2000US-02345859.
04-OCT-2000; 2000GB-00242633.
2000US-0180312.
                             2000US-0207456.
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2000US-0608408.
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2000GB-0024263.
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21-SEP-2000; 2000US-0234687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 TTCCTTGCTGGACAAC 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe of the invention.
                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                        measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                              The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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0
                                                                                                                                                                                                                                                                                               2.3%; Score 17; DB 22; Length 570;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain expressed single exon probe SEQ 1D NO: 11989.
                                                                                                                                                                                                                                                               Sequence 570 BP; 144 A; 142 C; 136 G; 148 T; 0 other;
                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                        Claim 1; SEQ LD No 9129; 530pp; English.
                                                                                                                                                                                                                                                                                                        100.0%; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAK11998 standard; DNA; 570 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
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30-JUN-2000; 2000US-0608408.
03-AU-2000; 2000US-0623466.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000US-024263.
           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00667.
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                                                                                                                                                                                                                                                                                                                                                                  167 TICCTIGCIGGACAAC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001 (first entry)
                                                                                                                                                                                                      congenital heart disease.
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss.
         Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483446/52.
                               WPI; 2001-488899/53.
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK11998;
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           Penn SG,
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                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid
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Example 4; SEQ ID NO: 11989; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%; Score 17; DB 22; Length 570;
100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 570 BP; 144 A; 142 C; 136 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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3U-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632566.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023687.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       550 TTCCTTGCTGGACAAAC 566
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ses 17; Conservative
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                                                                                                                                                                                                                                                                                                                         invention.
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Query Match

ô g AA118460;

AA118460/c

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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                          Probe #12263 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.3%; Score 17; DB 22; Length 570; 00.0%; Pred. No. 2e+02;
                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human placenta
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Matches 17; Conservative 0; Mismatches
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                       AAI43577 standard; DNA; 570 BP.
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26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023687.
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                                                                                                                  (first entry)
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                                                                                                                                                                                                                             genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                WO200157272-A2.
                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                    AAI43577;
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AA143577/C
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                              Probe #8393 for gene expression analysis in human cervical cell sample.
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                                               Gaps
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  2.3%; Score 17; DB 22; Length 570;
                                          0; Indels
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                     2e+02;
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                   100.0%; Pred. No. 2e+
ive 0; Mismatches
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                                                                                                                                                                                                                                           AA118460 Standard; DNA; 570 BP.
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30-JUN-2000; 2000US-0608408.
03-AGG-2000; 2000US-053866.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-OCT-2000; 2000GB-0024263.
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                                                                                     550 TTCCTTGCTGGACAAC 566
                                                                                                                                                                                                                                                                                                                                12-OCT-2001 (first entry)
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                                                                                                                                167 TTCCTTGCTGGACAAC 151
                     Best Local Similarity 100.8
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                cervical cancer; ss
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nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Penn SG,

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Gaps

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0; Indels

EP1074617-A2.

Query Match

Matches

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RESULT

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W0200151628-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length const. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length const allow obtaining of the full-length constants allow obtaining of the full-length constants are also useful for the AMH3633 to AMH3642 represent human constants.
                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprisising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises 3'-end sequence, where the polynucleotide which comprises 3'-end sequence, where the oligonucleotide comprises sa'-end sequence, where the oligonucleotide comprises sa'-end sequence, where the oligonucleotide comprises all east 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length oDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                              Yamamoto J;
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                             ashi K, Saito K, Y.
Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 751 BP; 160 A; 195 C; 199 G; 193 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast cancer expressed polynucleotide 17482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 1629; 2537pp + CD ROM; English.
                                                                                                                                                                           Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                           sogai T, Nishikawa T, Hay
Sugiyama T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pr
ative 0;
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                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                             28-JUL-2000; 2000EP-0116126.
                                                          99JP-0248036.
                                                                                                                    09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 cactgtatcetecetge 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention.
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Matches 17; Conservative
                                                                                                                                               (HELI-) HELIX RES INST.
                                                                                                                                                                                                                       WPI; 2001-318749/34.
                                                                                                                                                                             Isogai T,
                                                                                      L1-JAN-2000;
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                                                                                                      02-MAY-2000;
                                                          29-JUL-1999;
                                                                                                                                                                             Ota T, IS
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL25025;
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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ' cDNA sequence of prostate tumour clone J1-21.
                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                   Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 3228; 3695pp; English.
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100.0%; Pre
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97US-0806099.
97US-0904804.
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                                                                                                                                  2000US-0189167.
2000US-0192099.
                                                                                                                                                                                      29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-02530.
09-JUN-2000; 2000US-021315.
25-JUL-2000; 2000US-0220534.
                                                    10-JAN-2001; 2001WO-US00798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AGGAAGCTGAGAAATTG 130
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nes 17; Conserva
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                                                                                                                                                                  24-MAR-2000;
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                                                                                                                                     14-MAR-2000;
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                                                                                                           14-JAN-2000;
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19-JUL-2001
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us-10-020-139-1\_copy\_48\_793.oli.rng

Length 789;

Seguence 789 BP; 129 A; 240 C; 159 G; 195 T; 66 other;

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14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1998;
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                                                                                                                                                                                                                                                             AAA06272;
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                                 Query Match
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Matches
                                                                                                                                                                                          RESULT 74
                                                                                                                                                                                                         AAA06272/c
                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.
                                                                                                                         of a prostate tumour protein. The encoded immunogen, or the DNA itself can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour CDNA expression library with a normal tissue cDNA library with a normal
                                                                                                                                                                                                                                                                                                                                  Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
                                                                                                                   The present sequence is a DNA which encodes an immunogenic portion
                               Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate tumour specific gene; human; prostate cancer; detection;
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                             2.3%; Score 17; DB 19; Length 789;
100.0%; Pred. No. 2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Sequence 789 BP; 129 A; 240 C; 159 G; 195 T; 66 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3' fragment of prostate tumour specific gene J1-21.
                                                                                     Claim 12; Page 48; 130pp; English.
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97US-0904809.
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                                                                                                                                                                                                                                                                                                                                                                                    131 AGCCTGTTGCCGTCCTG 115
                                                                                                                                                                                                                                                                                                                                                                  498 AGCCTGTTGCCGTCCTG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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WPI; 1998-609886/51
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01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 - AUG - 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV58509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and belong them, antigen presenting cells which express the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as a probe or to modulate the expression of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06641 to AAA80691 and AAA82000 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated polypeptides, comprising an
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; diagnosis; tumour; gene therapy; detection; immunogenic; cytostatic; vaccine; ss.
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100.0%; Pred. No. 2e+02;
Live 0; Mismatches 0; Indels
                                                                               0; Indels
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                  Score 17; DB 19;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu J,
                                                                               Mismatches
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2.3%; Scc.
100.0%; Pre
0; '
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99US-0232880.
99US-0288946.
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98US-0159812.
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                                                                                                                                           498 AGCCTGTTGCCGTCCTG 514
                                                                                                                                                                                                    131 AGCCTGTTGCCGTCCTG 115
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nes 17; Conservative
                                                                                  Conservative
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polymucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes antibodies raised against the polypeptides (or antigenic epitopes form them) and antigenerseatting calls expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting calls are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer - \,
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                                                                                                                                                                                                                                                                      Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
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100.0%; Pred. No. 2e+02;
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Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Li Sx, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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                                                                                                                                                                                                                                   Human prostate cDNA sequence #32.
                                                                                                                         AAS63480 standard: cDNA; 789 BP.
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12-MAY-2000; 2000US-0568100.
13-JUN-2000; 2000US-0570737.
27-JUN-2000; 2000US-0693793.
27-JUN-2000; 2000US-065783.
10-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-0CT-2000; 2000US-0679426.
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APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMAR REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3'KINASE
        TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/972,629
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                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PROCR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, or CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,631
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Halluin, Albert P.
REGISTRATION UNDRER: 25,278
REPERENCE/DOCKET NUMBER: 8549-
TELECOMMUNICATION INFORMATION:
TELEFANE: (415,984-3660
IELEFAN: (415,984-3660
INFORMATION FOR SEQ ID NO: 1:
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Patent No. 5859201
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
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ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
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Best Local Similarity 100.0
Matches 20, Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: California
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Sequence 4, Appli
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                                                                                                                                                                                                                                                                                       APPLICANT: Stephens, Len
APPLICANT: Stephens, Len
APPLICANT: Harkins, Philip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
CORRESPONDENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows
SOFTWARE: FastSED for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUC-1997
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27-UN-1996
ATTORNEY AGENT INFORMATION:
US-09-479-776-11
US-09-060-756-178
US-09-586-125-1
US-08-282-581-4
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APPLICANT: Stephens, Len
APPLICANT: Hawkins, Dillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 8549-0006-999
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                               Sequence 1, Application US/08916917
Patent No. 5856132
GENERAL INFORMATION:
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; Patent No. 5856133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2448 ATCTTCATCCACTCCCTGGA 2467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                           RESULT 1
US-08-916-917-1
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100.0%; Pred. No. 1.1;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stephens, Len
TILLE OF INVENTION: PHOLINAL REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINGSITOL 3' KINASE
TITLE OF INVENTION: PHOSPHATIDYLINGSITOL 3' KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/972,630
                                                                                                                          8549-0005-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-972-630-1
Sequence 1, Application US/08972630
Patent No. 5869271
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REPRENCE/POCKET NUMBER: 8549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2448 ATCTTCATCCACTCCCTGGA 2467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665 ATCTTCATCCACTCCCTGGA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                    SS: single
unknown
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
US-08-972-629-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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US-08-972-630-1
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100.0%; Pred. No. 1.1;
    2.7%; Score 20; DB 2; Length 4692;
100.0%; Pred. No. 1.1;
                                             0; Indels
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APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TILLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
                                                                                                                                                                                                                                                                                     APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
ATILE OF INVENTION: GEBTA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL.3' KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,211 FILING DATE: 27-JUN-1996 CLASSIFICATION: 514
          100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1.1 Best Local Soli, Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     US-08-672-211-1
; Sequence 1, Application US/08672211
; Patent No. 5874273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09225170
Patent No. 6017763
                                                                                                                            2448 ATCITCAICCACTCCCTGGA 2467
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25,277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2448 ATCTTCATCCACTCCCTGGA 2467
                                                                                   665 ATCTTCATCCACTCCTGGA 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : (415)854-3660
(415)854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Halluin, Albert P. REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4692 base pairs
Query Match
Best Local Similarity 100.C
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: 1
STATE:
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100.0%; Pred. no.
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NUMBER OF SEQ 1D NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                        GH-70228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09300985A; Patent No. 6232441; GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,152
FILLING DATE: 19-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 32, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
                                                                                                   23,031
                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1986 GGCCCATCATTGGCCAGA 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1986 GGCCCATCATTGGCCAGA 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun APPLICANT: Dillin, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HURLE, MARK ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 GGCCCATCATTGGCCAGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 GGCCCATCATTGGCCAGA 428
                                                                                                                                                                                              TELEX: 846169
INFORMATION FOR SEQ 1D NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2345 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TRUNEH, ALEMSEGED
                                                                              NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: HOMO SAPIENS
US-09-300-985-1
                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear;
; MOLECULE TYPE: CDNA
US-08-955-937A-1
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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US-09-020-956-32/c
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GENERAL INFORMATION:

APPLICANT: WW, SHUJIAN

APPLICANT: WEST, RAYMOND

APPLICANT: SWEST, RAYMOND

APPLICANT: TUNENH, ALEMSEGED

TITLE OF INVENTION: GENE SUPERFAMILY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSE: RAINER & PRESTIA

STREET: PO. BOX 980

CITY: VALLEY FORGE
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PSSISEM: Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8549-0006-999
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/955,937A FILING DATE: 17-OCT-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    AFFLACTION DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
OFFICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-955-937A-1/c
; Sequence 1, Application US/08955937A
; Patent No. 6020161
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 8549
TELECOMUNICATION INDORMATION:
TELEPHONE: 650-493-4935
TELERAX: 650-493-5566
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1;
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                        30,605
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FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
  NUMBER OF SEQUENCES:
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                                                                                                                  COUNTRY: USA
ZIP: 10036-2811
                                                    STREET: 1100 ...
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US-09-225-170-1
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100.0%; Pred. No. 10;
tive 0; Mismatches 0; Indels
2.4%; Score 18; DB 3; Length 2345; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE TITLE OF INVENTION: SUPERFAMILY FILE OF INVENTION: SUPERFAMILY FILE REPERENCE: GH-70228-1 CORRENT APPLICATION NUMBER: US/09/300,985A CURRENT FILING DATE: 1999-04-28 EARLIER APPLICATION NUMBER: US 08/955,937 EARLIER FILING DATE: 1997-10-22 EARLIER APPLICATION NUMBER: US 08/055,152
                                                        0; Indels
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                                                                                                                                                                                                                                                                                         2.3%; Score 17; DB 4; Length 789; 100.0%; Pred. No. 32; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09439313 Patent No. 6329505
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LOCATION: (1)...(789)
COTER INFORMATION: n = A,T,C or G
US-09-439-313-32
         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
                                                                        32:
                         (206) 622-4900
(206) 682-6031
                                       INFORMATION FOR SEQ ID NO: 35 SEQUENCE CHARACTERISTICS: LEGUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHITE, Owen R. FRASER, Claire M.
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Best Local Similarity 100.0
Matches 17, Conservative
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APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-030-607-32
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                              TELEPHONE:
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LENGTH: 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%; Score 17; DB 4; Length 789;
100.0%; Pred. No. 32;
tive 0; Mismatches 0; Indels
                  NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patenth Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                            210121.427C2
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NAME: Maki, David J.
SEGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
                                                                                                                                                                                                                                                                                                                            us/09/020,956
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 6262245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/FOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 620-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: NUCLEIC acid
STRANDENESS: single
                                                                                                                                                                                                                                      COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               09-FEB-1998
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Best Local Similarity 100.0
Marches 17; Conservative
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: 09-FEI
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                            STREET: bocc CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 CC
CITY: Seattle
STATE: WA
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CLASSIFICATION:
                                                                                                                                                       USA
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                                                                                                                                              COUNTRY: US
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FEATURE:
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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GENERAL INFORMATION:
APPLICANT: Panula, Pertti A.J.
APPLICANT: Branch, Anniba
APPLICANT: Westerlund, Johanna
TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
FITLE OF INVENTION: Or therapy and diagnosis
FILE REFERENCE: 2530-104
CURRENT APPLICATION NUMBER: US/09/534,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.3%; Score 17; DB 4; Length 4403765; 100.0%; Pred. No. 29; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: Patentin Ver. 2.1
                                                                     FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEC ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37kv
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09534638
Patent No. 6320038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 1139230 tgttgccgtcctgggaga 1139247
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Best Local Similarity 100.0'
Matches 18; Conservative
                                                                                                                                                                                                                             LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4411529
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegei, Robert
APPLICANT: Schlegei, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred ...
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CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
SARLIER FILING DATE: 1998-06-10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO.142
CURRENT FILING DATE: 2000-03-27
EARLIER APPLICATION NUMBER: 09/365755
EARLIER FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catho, Theodore J.
APPLICANT: Pord, Donna M.
APPLICANT: Ford, Donna M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 AGCACTGTATCCTCCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                            617 AGCACTGTATCCTCCC 632
                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                 ; LOCATION: (7)..(393)
US-09-534-638-4
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                  ORGANISM: Mouse
                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-328-111-142
                                                                                                                                        396
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                                                                                                                                                               TYPE: DNA
                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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TITLE OF INVENTION: 123 Human Secreted Proteins FILE REFERENCE: P2010P1 CURRENT APPLICATION NUMBER: US/09/227,357
                                                                                                      CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER PLING DATE: 1997-07-08
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R APPLICATION NUMBER: 60/055,950
R FILING DATE: 1997-08-18
R PELLING DATE: 1997-08-18
R FILING DATE: 1997-08-18
R APPLICATION NUMBER: 60/055,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/058,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFFLING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,916
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,930
FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/051,918
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,920
APPLICATION NUMBER: 60/051,930
APPLICATION NUMBER: 60/052,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER: 60/052,733
1997-07-08
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1997-08-18
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,732
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,931
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/055,723
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APPLICATION NUMBER: 60/055,949
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APPLICATION NUMBER: 60/055,984
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FILING DATE: 1997-09-12
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APPLICATION NUMBER: 60/058,664
                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/051,929
                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,803
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/051,932
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                GENERAL INFORMATION:
APPLICANT: Fischer et al.
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Patent No. 6342581
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Gey
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                         LOCATION: (376)
COTHER INFORMATION: n equals a,t,q, or c
US-09-227-357-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MA-703C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42, Application US/08844188 Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Narva, Kenneth E.
Schnepf, H. Ernest
Knuth, Mark
Pollard, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39,355
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA (genomic) US-08-844-188-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 1152 base pairs
nucleic acid
EDNESS: single
NUMBER OF SEQ 1D NOS: 672
SOFTWARE: Patentin Ver. 2:0
SEQ 1D NO 87
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                       545 TCACTTTCCTTGCTGG 560
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 352-372-5800 INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sanders, Jay M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 19-API
                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Narva,
APPLICANT: Schnepf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-844-188-42
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STATE:
                                                                                                                       FEATURE:
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2.1%; Score 16; DB 3; Length 1152;

Query Match

us-10-020-139-1\_copy\_48\_793.oli.rni

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2.1%; Score 16; DB 2; Length 1493; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/801,863 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: $30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHORE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 4:
                                                                           ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: C/O FISH & NEAVE STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/486,596A FILING DATE: JUNE 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN
                   TITLE OF INVENTION: ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, HISAYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity 100.9
Matches 16; Conservative
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TITLE OF INVENTION: ADRE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: double
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                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
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US-08-486-596A-4/c
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                                  Gaps
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Pred. No. le+02;
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APPLICATION NUMBER: US/08/233,389C
                 Best Local Similarity 100.0%; Pred. No. 1e+4
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                           APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAMA, Kenji
APPLICANT: MATSOO, Hisayuki
APPLICANT: ETO, Tanenao
ITTLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: HALEY Jr., James F.
RECISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                Sequence 4, Application US/08233389C Patent No. 5639855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
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TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1493 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAMA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
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                                                                                                     1039 CCAAATCATCAACAAG 1054
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                                                                             571 CCAAATCATCAACAAG 586
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Matches 16; Conservative
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148..711
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STRANDEDNESS: doub
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US-08-233-389C-4
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APPLICANT: Tang, Y. Tom
APPLICANT: Tue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Ghah, Purvi
TITLE OF INVENTION: HOMAN GROWTH-ASSOCIATED METHYLTRANSFERASE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 16; DB 3; Length 2057; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                    Length 1493;
                                                                                                                                                           Query Match 2.1%; Score 16; DB 2; Length 1495
Best Local Similarity 100.0%; Pred. No. 1e:02;
Matches 16; Conservative 0; Mismatches 0; Indels
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PILLING DATE: """
FILING DATE: """
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F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF-0495 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-059-522-2; Sequence 2, Application US/09059522; Patent No. 6001607
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TELEPHONE: 650-855-0555
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cerrone, Michael REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 GCCAAGCAGAAGGCCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                        645 CIGGGACCICAGAGIC 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 GCCAAGCAGAAGGCCC 233
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TELEFAX: 650-845-4166
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; LOCATION: 148..711
US-09-004-713-4
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; CLONE: 2496002
US-09-059-522-2
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STATE:
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100.0%; Pred. No. 1e+02;
.ive 0; Mismatches 0; Indels
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NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 77,794
REFRENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
                                                                                                                                                  REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 595-9000
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Sequence 4, Application US/09004713
Sequence 4,
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1251 Avenue of the Americas
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FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
                                                                               NAME: HALEY Jr., James F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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TELEFAX: (212) 596-9090
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                     ATTORNEY/AGENT INFORMATION:
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Matches 16; Conservative
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STRANDEDNESS: double
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; LOCATION; 148..711
US-08-486-596A-4
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             CLASSIFICATION:
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Nucleic Acid Coding for the Human
TestLoular Angiotensin Converting Enzyme (ACE) and its
Uses, Especially for the In Vitro Screening for this
Enzyme in the Organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 16; DB 3; Length 213; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
  2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/633,993
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/481,626
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                 MA-703C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alhenc-Gelas, Francois
APPLICANT: Hubert, Christine
APPLICANT: Corvol, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08481626
; Patent No. 5801040
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sanders, Jay M. RECISTRATION NUMBER: 39,355 REFERENCE/DOCKET NUMBER: MA TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2132 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 352-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TEST
TITLE OF INVENTION: Uses
TITLE OF INVENTION: Enzy
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                          ZIP: 32606-6669
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                     Gainesville
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                                                             USA
                                                                                                                        MEDIUM TYPE:
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US-08-481-626-1/c
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                                                             COUNTRY:
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STREET:
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                                           STATE:
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                                     Patent No. 613274

GENERAL INFORMATION:
APPLICANT: Yang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
TITLE OF INVENTION:
HUMAN GROWTH-ASSOCIATED METHYLTRANSFERASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 16; DB 3; Length 2057; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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APPLICANT: Knuth, Mark
APPLICANT: Knuth, Mark
APPLICANT: Cardineau, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
CARRESPONDENCE ADDRESS:
CADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS SOFTWARE EASLEGG for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/382,027
                                                                                                                                                                                                                        SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0495 US
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/059,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/08844188; Patent No. 6127180; GENERAL INFORMATION:
  US-09-382-027-2
; Sequence 2, Application US/09382027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Narva, Kenneth E. APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2057 base pairs TYPE: nucleic acid STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                    S: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-382-027-2
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                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                               94304
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APPLICANT: Donald C. Foster
APPLICANT: Frank J. Grant
APPLICANT: Clindy A. Sprecher
TITLE OF INVENTION: HEMATOPOLETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,740
                                                                                                                                                                                                NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 04958-0006-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
                                           APPLICATION NUMBER: US 07/656,183
FILING DATE: 04 WAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenelics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                               APPLICATION NUMBER: FR 89-09062
FILING DATE: 05-JUL-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08653740 Patent No. 5792850
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NAME: Parker, Gary E
RECISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
US-08-481-626-1
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERESTICS: LENGTH: 2589 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                        ::
                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ 1D NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2478 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2049 AGGCCCAGGAAGCTGA 2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AGGCCCAGGAAGCTGA 246
                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                         2.1%; Score 16; DB 1; Length 2589; diarity 100.0%; Pred. No. 1e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: James W. Baumgartner
APPLICANT: James W. Baumgartner
APPLICANT: Frank J. Grant
APPLICANT: Frank J. Grant
APPLICANT: Clindy A. Spreecher
ITILE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/073,594
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              US-09-073-594-6; Sequence 6, Application US/09073594; Patent No. 5925735; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-442 OF INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                 2225 ATCCTCCTGCTGCAG 2240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                11..1882
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                   MOLECULE TYPE: CDNA
                                                                                                                                                                                 Best Local Similarity
Matches 16; Conserv
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linear
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CLASSIFICATION:
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                                                          ) NAME/KEY:
) LOCATION:
US-08-653-740-6
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US-09-073-594-6
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                                                                                                                                                                Query Match
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Sequence 3, Application US/08968751
Patent No. 5948643
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3155 base pairs
                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                Z1P: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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                                                                                                            OPERATING SYSTEM:
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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                    USA
                                                                                                                                                                                      FILING DATE
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US-09-442-100-7
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                                                                                                                                SOFTWARE:
                                                                                          COMPUTER:
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                    COUNTRY:
STATE:
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Patent No. 6359193
APPLICANT: Xu, Tian
APPLICANT: Tao, Widan
APPLICANT: Tao, Weiyi
APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVENTION: UUCLEOTIDE AND PROFEIN SEQUENCES OF LATS
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2589;
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                                                                                APPLICANT: James W. Baumgartner
APPLICANT: Donald C. Foster
APPLICANT: Frank J. Grant
APPLICANT: Clindy A. Sprecher
TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/275,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                        ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95-31
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NAME: PATKET, GALY
REGISTRATION NUMBER: 3,648
REFERENCE/DOCKET NUMBER: 95-31
TELECHONNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEPHONE: 206-442-6673
                                Sequence 6, Application US/09275925 Patent No. 6080406
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                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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LENGTH: 2589 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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nes 16; Conserva
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                                                                        GENERAL INFORMATION:
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US-09-442-100-7/c
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                    US-09-275-925-6
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RESULT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
E: Floppy disk
IBM PC Compartible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rubinfeld, Bonnee
APPLICANT: Polakis, Paul G.
APPLICANT: Ligenfelter, Carol
APPLICANT: Voong, Terilyn T.
TITLE OF INVENTION: MODULATORS OF BRCAI ACTIVITY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. le+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ONYX Pharmaceuticals, Inc. STREET: 3031 Research Drive CITY: Richmond
                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                                                                                                                                                                                                                                                                      6523-003
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                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
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Gaps

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Score 16; DB 1; Length 3565;
Pred. No. 1.1e+02;
                                                                 0; Indels
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2.1%; Score 16; DB 5; Le
Best Local Similarity 100.0%; Pred. no. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0;
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                                                                   Mismatches
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Patent No. 6197505
GENERAL INFORMATION:
APPLICANT: No. 6197505berg, Leif T
APPLICANT: Andersson, Maria K
APPLICANT: Linstrom, Per H
            2.1%; Scc.
100.0%; Pre
0; 1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                              1055 TCCCTCATCCTGGATG 1040
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LENGTH: 3565 base pairs
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                         Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                         320 TCCCTCATCCTGGATG 335
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FILING DATE: 199306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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Sequence 44, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: CALABATELLA, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLICONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 16; DB 2; Length 3256; 100.0%; Pred. No. 1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5: Seidel, Gonda, Lavorgna & Monaco, P.C.
Two Penn Center, Suite 1800
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MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
NAME: Glotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: 0NYX1024 GG
TELECOMMUNICATION INFORMATION:
TELECHONE: (510) 262-8710
TELETAX: (510) 222-9758
INFORMATION FOR SEQ 10 NO: 3:
SEQUENCE CHRACTERIST(CS:
LENGTH: 3256 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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N: 514
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 832
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEFX: 0. 57340339e
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
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OPERATING SYSTEM: MS-DOS
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Matches 16; Conservative
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EDNESS: double
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PRIOR APPLICATION DATA:
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U.S.A.
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                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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US-08-968-751-3
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pCT-US93-06251-20/c

Sequence 20, Application PC/TUS9306251

GENERAL INFORMATION:

APPLICANT: Wickstrom, Eric and Rife, Jason P.

TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF FILE REFERENCE: 1248/1DoyS.
CURRENT APPLICATION NUMBER: US/09/050,159A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Patent No. 6248724

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANN: Phillips, M. Ian
APPLICANN: Phillips, M. Ian
APPLICANN: Phillips, M. Ian
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED TO
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME MRNA AND METHODS OF USE
FILE REFERENCE: UFCA.1087/UFLA.0877

CURRENT APPLICATION NUMBER: 05/09/162,484
CURRENT RAPLICATION NUMBER: 60/059,661

EARLIER APPLICATION NUMBER: 60/059,661

EARLIER APPLICATION NUMBER: 60/059,661

EARLIER PRINT ON OS: 19
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                         2.1%; Score 16; DB 4; Length 4020; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 16; DB 4; Length 402.
100.0%; Pred. No. 1.1e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    ; OTHER INFORMATION: Angiotensin I converting enzyme mRNA
US-09-050-159-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbon Ape Leukemia Virus-Based
Retroviral Vectors
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SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/716,351A
FILING DATE:
CURRENT FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/042,930
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; Patent No. 6033905
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                                       EARLIER FILING DATE: 1987-04-03
NUMBER OF SEQ ID NOS: 133
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 130
LENGTH: 4020
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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ORGANISM: Homo sapiens
                                                                                                                                                                                       ORGANISM: Homo sapiens
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US-08-716-351A-1/C
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                                                                                                                                                                 · TYPE: DNA
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APPLICANT: Panula, Pertti A.J.
APPLICANT: Brandt, Annika
APPLICANT: Beretriund, Johanna
APPLICANT: Westerfund, Johanna
TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
TITLE OF INVENTION: for therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                15280-128-1PC
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CURRENT APPLICATION NUMBER: US/09/534,638
CURRENT FILING DATE: 2000-03-27
CARLIER APPLICATION NUMBER: 09/365755
EARLIER FILING DATE: 1999-08-03
NUMBER OF SEQ 10 NOS: 22
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 626546
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
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; Sequence 1, Application US/09534638
; Patent No. 6320038
                                                                                                                                                                                      TELEPHONE: (415) 543-6600
TELEFAX: (415) 543-5643
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ELNGTH: 8535 base pairs
TYPE: nucleic acid
                                                                                                NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774 REFERENCE/DOCKET NUMBER: 15, TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                           single
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ORGANISM: Mouse
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FEATURE: OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0;
       EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION WOMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 578
SOFTWARE: PALENT.pm
SEQ ID NO 183
LENGTH: 37950
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APPLICANT: FLEISCHMAN, ROBERT D.
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LOCATION: 23387..23510
OTHER INFORMATION: exon7
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OTHER INFORMATION: exon4
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                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                           LOCATION: 12675..12791
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LOCATION: 19822..19912
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LOCATION: 21789..21950
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LOCATION: 25520..26016
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LOCATION: 5259.:5328
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LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
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US-09-103-840A-2/C
                                                                                                                                                               TYPE: DNA
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APPLICANT: Blumenfeld, Marta
APPLICANT: 11ya, Chumakov
APPLICANT: 11ya, Chumakov
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18CP1CP
CURRENT APPLICATION NUMBER: US/09/338,907
CURRENT FILING DATE: 1999-06-23
EARLIER FILING DATE: 1999-06-23
EARLIER FILING DATE: 1999-06-29
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
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APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate cancer gene
CILER REFERENCE: GENSET: 018CP1
CURRENT APPLICATION NUMBER: US/09/218,207
CURRENT FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 08/996,306
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Patent No. 6346381
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
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LOCATION: 25520..26016
CTHER INFORMATION: exon8
US-09-338-907-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: exon3
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                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 12675..12791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14621..14710
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LOCATION: 19822..19912
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LOCATION: 21789..21950
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Matches 16; Conserva
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NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
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1 AGUGCUUGGCAACUG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-435-628-128
                                                                                                        US-08-435-628-128
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                                                                                    RESULT
                       Ωp
                                                                                                        Gaps
                                                                                                     0;
                                                        2.1%; Score 16; DB 4; Length 4403765; 100.0%; Pred. No. 50; tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Drayes, James
APPLICANT: Dravis, Thate
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR
TILE OF INVENTION: TREATMENT OF RESTENOSIS AND
TILE OF INVENTION: CANCER USING RIBOZYMES
CORRESPONDENCES: 2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
SYSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JMBER: US/08/373,124A
January 13, 1995
                                                                                                                                                                                                                                                           US-08-373-124A-128
; Sequence 128, Application US/08373124A
; Patent No. 5646042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192, 943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/245,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                               Db 1708955 CTGAGAAATTGCTGAA 1708940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,327
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3310
INFORMATION FOR SEQ ID NO: 128
                                                                                                                                          243 CTGAGAAATTGCTGAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                   Conservative
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Best Local Similarity 73.3°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                              Best Local Similarity
Matches 16; Conserv
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US-08-373-124A-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
US-09-: 03-840A-2
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                                                          Query Match
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Gaps
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                    Patent No. 581/720

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHONS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENGIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
TITLE OF INVENTION: CANCER USING RIBOZYMES
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. DOS 5.0 SOTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628 FILING DATE: 05-MAY-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UMBER: ..., 1994
February 7, 1994
WIMBER: 07/987,132
Sequence 128, Application US/08435628 Patent No. 5817796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            January 13, 1995
JMBER: 08/245,466
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                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/373,124
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: August 26, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.0°
Best Local Similarity 73.3°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACUGCUUGGCAACUG 15
                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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RESULT 42

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206 AGTGCTTGGCAACTG 220

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0; Mismatches
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AFTING DATE: 10-DEC-1991
AFTORNEY AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
NAME: DOYLE LEARY Ph.D., KATHRYN
NAME: MIMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROCKOP, DARWIN J.
SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08943731 Patent No. 6265157 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEREDA, LARISA
LARSON, ANDREA W.
PACK, MICHAEL
COLIGE, ALAIN
EARLY, JAMES
KORKKO, JARMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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; MOLECULE TYPE: DNA (genomic)
US-08-943-731-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
                                                                                                                                                                                 Query Match 2.0%
Best Local Similarity 100.0
Matches 15; Conservative
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TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 227 base pairs
                                                                                                                                                                                                                                                                                 571 CCAAATCATCAACAA 585
                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               46 CCAAATCATCAACAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHILADELPHIA
                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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ZIP: 19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                        US-08-477-928A-43
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US-08-943-731-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                    ò
                                                             GENERAL INCORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: STINCHCOMB, JAMES A.
APPLICANT: STINCHCOMB, DAN T.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: UNCONDITIONS WELATED TO LEVELS OF C-FOS
FILE REFERENCE: 231/75
CURRENT APPLICATION NUMBER: US/08/998,099A
CURRENT FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-33
EARLIER FILING DATE: 1997-01-33
EARLIER FILING DATE: 1997-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43, Application US/08477928A
Patent No. 6207389
GENERAL INFORMATION:
APPLICANT: Dosch, Hans M.
TITLE OF INVENTION: METHODS FOR CONTROLLING T
TITLE OF INVENTION: METHODS FOR CONTROLLING T
APPLICANT: APPROACH METHODS FOR CONTROLLING T
MUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Score 15; DB 3; Length 50; 86.7%; Pred. No. 2.9e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,928A FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthesized Hairpin Ribozyme US-08-998-099-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1299 Pennsylvania Avenue
CITY: Washington D.C.
STATE: Callifornia
COUNTRY: U.S.A.
ZIP: 20004-2400
COMUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS
STREET: 1299 Pennsylvania Avenue
                     Sequence 289, Application US/08998099A Patent No. 6103890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/COCKET NUMBER: 19,
TELECOMMUNICATION INFORMATION:
TELEPHONE: ///
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 639 7700
TELEFAX: (202) 639 7890
INFOREMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.09
Best Local Similarity 86.79
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 TGCTGCAGAAGGAGA 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
US-08-477-928A-43
US-08-998-099-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fas
SEQ ID NO 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
                                                     Patent No.
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APPLICANT: ALA-KOKKO, LEENA, et al. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                               .;
0
2.0%; Score 15; DB 4; Length B1; 100.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWAKZE JACOBS 6 NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/943,731
FILING DATE: 03-0CT-1997
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF
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                                                                                                                                                                                                                                                                                                                                       Length 456;
                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                  2.0%; Score 15; DB 2; Le
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
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                                                              210121.422
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15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Sequence 16, Application US/08834306
; Patent No. 6054135
                                                         REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                        31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION:
                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 16:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 16:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 2.0%
Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   633 TGCTGCAGAAGGAGA 647
                      NAME: Maki, David J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TGCTGCAGAAGGAGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 15; Conserva
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                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-557-309B-16
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US-08-834-306-16
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT PAPLICATION NUMBER: 05/081,280
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER PILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-01-10
NUMBER OF SEQ ID NOS: 224
SOUTHARD APPLICATION NUMBER: 60/028,550
EARLIER PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOUTHARD: 1996-10-11
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: anti-Rh(D) antibody clone SH28, SH50, and SH53 US-09-240-274-189
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                                   Length 227;
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                          Match 2.0%; Score 15; DB 4; Length 227 Local Similarity 100.0%; Pred. No. 3.1e+02; les 15; Conservative 0; Mismatches 0; Indels
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CHARLICATION NUMBER: US/08/557,309B FILING DATE: 14 NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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14-NOV-1995
                                                                                                                                                                                                                                                           Sequence 189, Application US/09240274 Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08557309B Patent No. 5916572
                                                                                                                                          105 TGGGACCTCAGAGTC 119
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Matches 15; Conservative
                                                                                                                 46 TGGGACCTCAGAGTC 60
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                   RESULT 45
US-09-240-274-189
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                                 Query Match
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Gaps
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APPLICANT: NERDUKRAK, VIVEK R.
APPLICANT: JENKINS, CAROL
APPLICANT: JENKINS, CAROL
APPLICANT: MILLER, MARK
TITLE OF INVENTION: PAPUA NEW GUINEA HUMAN T-LYMPHOTROPIC
TITLE OF INVENTION: VIRUS
                                                                                                                                                                                                         Query Match 2.0%; Score 15; DB 4; Length 495; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0; Indels
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PatentIn Release #1.0, Version #1.25
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                                                                                 NAME/KEY: exon
LOCATION: (111)..(224)
OTHER INFORMATION: n is G or A or C or T/U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/07743518; Patent No. 5397696; GENERAL INFORMATION:
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IBM PC compatible
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TELEFAX: 202-822-0944
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 520 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                      246 AGAAATTGCTGAACA, 260
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                                                                                                                                                                                                                                                                                                                             ZIP: Z0036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AACTCCCTCATCCTG 19
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CLASSIFICATION: 424
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                                       ORGANISM: Homo sapiens
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                                                                                                                                                 US-09-323-472A-5
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LENGTH: 495
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APPLICANT: Summar, Marshall
APPLICANT: Summar, Marshall
APPLICANT: Christman, Brian
TITLE OF INVENTION: HUMAN CARBAMYL PHOSPHATE SYNTHETASE I POLYMORPHISM AND DIAGNOST
TITLE OF INVENTION: THERAPEUTIC METHODS RELATING THERETO
FILE REFERENCE: 1242/19
                                                                                                                                                                                                                                                                                                                        PREVENTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                       APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: MILH, John M.
APPLICANT: MCHall, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%; Score 15; DB 4; Length 456; 100.0%; Pred. No. 3.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210121.422C2
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18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             Sequence 16, Application US/08993674A Patent No. 6228372 GENERAL INFORMATION:
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; Sequence 5, Application US/09323472A
; Patent No. 6346382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Best Local Similarity 100.
Matches 15; Conservative
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                    3 TGCTGCAGAAGGAGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 18-DEC
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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US-08-993-674A-16
                                                                                                     US-08-993-674A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 5
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20002
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US-08-803-899-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 231
LENGTH: 601
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APPLICANT: DONAHOE, PATRICIA K.
APPLICANT: WANG, TONGWEN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES TITLE OF INVENTION: ENCODING THEM NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%; Score 15; DB 2; Length 553; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,488
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             US-08-721-488-7; Sequence 7, Application US/08721488; Patent No. 5965388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brown. Scott A.
REGISTRATION NUMBER: 32.724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 498-8224
INFORMATION FOR SEC ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-803-899-1/c
; Sequence 1, Application US/08803899
; Patent No. 5912224
                                                                                                                                                                                 APPLICANT: Merberg, David
APPLICANT: Treacy, maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
                                                                                                                    McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                            GENERAL INFORMATION:
   APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                         Abb...
STREET: 8/ C. CITY: Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100,0
es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 AGAAGGCCCAGGAAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 AGAAGGCCCAGGAAG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-721-488-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          02140
                                                                                                                                                             APPLICANT:
                                                                                                                       APPLICANT:
                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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2.0%; Score 15; DB 2; Length 571; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803.899
FILIG DATE: 02/21/1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                   0609.4240001
                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/012,054
ELISING DATE: 02/22/1996
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: STEFFE ERIC K
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 231, Application US/09385982
Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(601)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEO 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 571 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 GCAACTCCCTCATCC 329
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                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
USA
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2.0%; Score 15; DB 1; Length 877; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
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TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                        APPLICANT: MATTHEW MOYLE, ET AL. TITLE OF INVENTION: NOVEL NEUTKOPHIL INHIBITORS NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: ISM Compatible
OOFRATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PEFFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/151,064
FILING DATE: 10.NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11.HAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24.DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11.HAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,158
SR: 205/073
                                      Sequence 95, Application US/08173510B Patent No. 5747296 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 93, Application US/08458218
; Patent No. 5789178
; GENERAL INFORMATION:
                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: Coding Sequence ; LOCATION: 1...822 US-08-173-510B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 AACCGATCGATGATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 AACCGATCGATGATG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: NUCLEIC
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEIC ACID
                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINEAR
                                                                                                                                                                                                                                                                                                                     U.S.A.
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                                                                                                                                                                                                                                                                                                                  COUNTRY: U
RESULT 55
US-08-173-510B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-458-218-93
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                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Renestine, Philipp
APPLICANT: Rechtch, Philipp
APPLICANT: Rechtch, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDERS: 1152
CORRESPONDERS: 1152
CORRESPONDERS: 1152
CORRESPONDERS: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.0%; Score 15; DB 4; Length 728; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                           2.0%; Score 15; DB 4; Length 601; 100.0%; Pred. No. 3.2e+02;
                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COINDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PE/5-30306/A/CCC1976
                                                       100.08; Pred. No. . . . . . 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwalls Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                            ; Sequence 604, Application US/08998416
; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 604:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PE. TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 728 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 919-541-8689
                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 AAGCAGAAGGCCCAG 238
                                                                                                                                     568 CAGCCAAATCATCAA 582
                                                                                                                                                                309 CAGCCAAATCATCAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATIÓN NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAG1412UP
                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                     RESULT 54
US-08-998-416-604/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM:
US-08-998-416-604
                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                            Matches
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Gaps

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Ouery Match 2.0%; Score 15; DB 2; Length 877; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ASADA, KIYOZO
APPLICANT: KATO, Ikunoshin
TITLE OE INVENTION: DAMA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
CURRENT APPLICATION NUMBER: US/09/446,504
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1997-06-26
PRIOR FILING DATE: 1997-06-26
PRIOR FILING DATE: 1997-06-27
PRIOR APPLICATION NUMBER: JP 9-320692
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                      COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
                                                                                                                                                                   PRIOR DATE:
PRIOR DATE:
APPLICATION NUMBER:
(08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER:
(08/16),064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/891,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205/073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/09446504; Patent No. 6218150
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUKAI, Hiroyuki
ASADA, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UEMORI, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUJITA, Tomoko
MIYAKE, Kazue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 AACCGATCGATGATG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AACCGATCGATGATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                       storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SATO, Yoshimi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1...822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: UEMORI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                       MEDIUM TYPE:
                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-450-497-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-446-504-4
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 95, Application US/08450497
Patent No. 5919900
GENERALINFORMATION:
GENERALINFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/458,218
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
ATTORNEY/AGENT INFORMATION:
  ADDRESSEE: Lyon & Lyon STREET: 633 West Fiith Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fiith Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 93:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: Coding Sequence
; LOCATION: 1...822
US-08-458-218-93
                                                                                                                                                                                                                          COMPUTER: IHM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AACCGATCGATGATG 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LINEAR MOLECULE TYPE: NUCLEIC
                                                                                                                                                          COMPUTER READABLE FURM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                    Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINEAR
                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                             COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-450-497-95
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PatentIn Ver. 2.1

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Gaps
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APPLICANT: Hellmann, Gary M.
APPLICANT: Gill, Laurence K.
APPLICANT: Kunagai, Monto H.
APPLICANT: Winagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
CORRESPONDENCES: 19
                                                                                                                                                                                                                                                                          Length 1192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1316;
                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
COUNTRY: No. 5705624th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 15; DB 1; Le
ilarity 100.0%; Pred. No. 3.2e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                            2.0%; Score 15; DB 4; L 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0;
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REGISTRATION NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/08579667
; Patent No. 5705624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        Query Match 2.0%
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                    445 CTCCTTGGACCTCCT 459
                                                                                                                                                                                                                                                                                                                                                                                                               146 etcettggacetect 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                ORGANISM: HOMO SAPIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..1239
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28234
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US-08-579-667-3/c
                                                                                                                                       1192
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                                                                                                                                                                                                         us-09-142-565-1
                                                                                                                                                               TYPE: DNA
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Best Local S
                                                                                                                                          LENGTH:
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                                                                                                                                                        2.0%; Score 15; DB 4; Length 984; 100.0%; Pred. No. 3.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.0%; Score 15; DB 4; Length 984; 100.0%; Pred. No. 3.2e+02; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, YOSHIMI
APPLICANT: SATO, YOSHIMI
APPLICANT: SATO, YOSHIMI
APPLICANT: MIVAE, Kazue
APPLICANT: MIVAE, Kazue
APPLICANT: MIVAI, HICOUKI
APPLICANT: MORAI, HICOUKI
APPLICANT: MARDA, IKUNOSHIN
TITLE OF INTENTION: DNA POLYMERASE-RELATED FACTORS
FILER REFERENCE: 1422-408PCT
CURRENT FALING DATE: 1909-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: UP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR PLING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: UP 9-320692
PRIOR APPLICATION NUMBER: UP 9-320692
PRIOR PLING DATE: 1997-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFRENCE: G43002
CURRENT APPLICATION NUMBER: U$/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09142565A
Patent No. 6187560
GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Rely Paine
APPLICANT: Robert James
                                                                                                                                                                                                                                                                                                                                                                                       US-09-712-266-4
; Sequence 4, Application US/09712266
; Patent No. 6333158
                                              TYPE: DNA CAGANISM: Pyrococcus furiosus US-09-446-504-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pyrococcus furiosus
US-09-712-266-4
                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Ver. 2.1
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                                                                                                                                                                                                                                                       637 GCAGAAGGAGATATG 651
                                                                                                                                                                                                                                                                                                601 gcagaaggagatalg 615
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Matches 15; Conserv
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       SEQ ID NO 4
LENGTH: 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                Dp
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TITLE OF INVENTION: METHIONINASE, PURIFIED RECOMBINANT METHIONINASE PRODUCED TITLE OF INVENTION: THEREFROM AND USES THEREOF NUMBER OF SEQUENCES: 8
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TITLE OF INVENTION: RECOMBINANT L-METHIONINE GAMMA-LYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.2e+02;
                                             ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%; Score 15; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 3.2 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0020-3989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/641,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/08642541
; Patent No. 5891704
                                                                                                                                                           ZIP: 22040-0747
COMPUTER READABLE FORM:
WEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1320 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      698 CAGCAGGTCGTCGAT 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double
                     NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
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61..1254
                                                                                                   FALLS CHURCH
                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                               FILING DATE:
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; LOCATION:
US-09-059-178-1
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                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT: SODA, KENJI
APPLICANT: TANAKA, HIDEHIKO
APPLICANT: INOUE, HIROYUKI
AFPLICANT: INOUE, HIROYUKI
AFPLICANT: INOUE, HIROYUKI
AFPLICANT: ESAKI, NOBUYOSHI
TITLE OF INVENTION: RECOMBINANT L-METHIONINE GAMMA-LYASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 15; DB 2; L6
100.0%; Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0020-3989
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5863788
GENERAL INFORMATION:
APPLICANT: TANAKA, HIDBHIKO
APPLICANT: INOUE, HIROVIKI
APPLICANT: INOUE, HIROVIKI
APPLICANT: INOUE, HIROVIKI
APPLICANT: ESAKI, NOBUYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
                                                                                                                                            US-08-641-038A-1/c
; Sequence 1, Application US/08641038A
; Patent No. 5861154
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURRHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0020
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1320 base pairs
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Best Local Similarity 100.
Marches 15, Conservative
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                                               490 CATCAACAAGTTCGT 476
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EDNESS: double
                         577 CATCAACAAGTICCT 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Cli.
STATE: V. COUNTRY: USA
TP. 22040-0747
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US-08-641-038A-1
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0; Mismatches
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FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09260889; Patent No. 6231854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 31:
TELLCOMMUNICATION INFORMATION:
DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Coding Sequence LOCATION: 48...1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/91
FILING DATE: 19-AUG-1997
APPLICATION NUMBER: 08/64
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202-822-0168
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                                                                                       2.0%
Best Local Similarity 100.0
Matches 15; Conservative
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EDNESS: double
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Z1P: 20006-1888
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2000
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Best Local Similarity
**+rhes 15; Conserv
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               ; ANTI-SENSE: YES
US-08-642-541-3
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1369;
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APPLICATION NUMBER: US/08/642,541
                                                                         NAME: Millman, Robert A.
REGISTRATION UNBER: 36,217
REFERENCE/COCKET NUMBER: 31276-20002.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31276-20002.21
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2000 Pennsylvania Avenue, NW
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03-MAY-1996
 APPLICATION NUMBER: US/08/642,541
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COMBUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 65
US-08-642-541-3
; Sequence 3, Application US/08642541
; Patent No. 5891704
; GENERAL INFORMATION:
APPLICANT: YUYING, TAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Millman, Robert A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION: INFORMATION:
                                                                                                                                               TELEFAX: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
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TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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                 03-MAY-1996
                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          698 CAGCAGGTCGTCGAT 712
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                     linear
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Matches 15; Conserve
                   FILING DATE: 03 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                     TOPO1.0GY:
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US-08-642-541-1
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Gaps
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2.0%; Score 15; DB 2; Length 1369; 100.0%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                          APPLICANT: TAN, YUYING
TITLE OF INVENTION: HIGH EXPRESSION MODULES ENCODING
TITLE OF INVENTION: METHIONINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOLKSILK
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.0%; Score 15; DB 4; Le 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
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                                                                          USA
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                                                                            COUNTRY:
                 STREET:
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Sequence 20, Application US/08174467
Sequence 20, Application US/0817467
Sequence 20, Application US/0817467
Sequence 20, Application US/0817467
SEMERAL INFORMATION:
APPLICANT: BOUDET, ALAIN M.
APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                         APPLICANT: TAN, YUYING
TITLE OF INVENTION: HIGH EXPRESSION MODULES ENCODING
TITLE OF INVENTION: METHIONINASE
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTEM: Windows SOFTWARE: FASTEQ for Windows Version 2.0b CURRENT APPLICATION DATA: US/09/260 non FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29,959
ER: 31276-20002.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/914,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-AUG-1997
APPLICATION NUMBER: 08/642,541
FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                              Sequence 3, Application US/09260889
Patent No. 6231854
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 31:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 200-887-1500
TELEFAX: 202-822-0168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Murashige, Kate H
REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100. Matches 15; Conservative
  1208 CAGCAGGTCGTCGAT 1194
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                      STREET: ZOUV.
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20006-1888
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US-09-260-889-3
                                                                               US-09-260-889-3
                                                                                                                                                                                                                                                                                                                     STATE:
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2.0%; Score 15; DB 1; Length 1377; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
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APPLICANT: INZE, DIRK G.
APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
UNMER OF SOUTENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,467
FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95563/PS36321/US
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166
FILING DATE: 27.ABF.1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N:
REGISTRATION NUMBER: 16,753
REFERENCE/DOCKET NUMBER: 95563/PS363
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERX: 202-80.3000
TELEFERX: 202-82-0944
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/874,166
                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 6066780
GENERAL INFORMATION:
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IBM PC compatible
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LENGTH: 1377 base pairs
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Best Local Similarity 100.0
Matches 15; Conservative
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STRANDEDNESS: single
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                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-174-467-20
                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                            WASHINGTON
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Length 1423;
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TITLE OF INVENTION: Pharmaceutical Composition For Use In
TITLE OF INVENTION: Treating Inflammation
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/829,954
FILING DATE: 19920203
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                    E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16777/160
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APPLICATION NUMBER: US 07/664,114
FILING DATE: 04-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/204,356
FILING DATE: 09-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/653,736
FILING DATE: 11-FBB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/204,400
FILING DATE: 09-JUN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      Sequence 1, Application US/07829954
Patent No. 5344819
GENEZI INFORMATION:
APPLICANT: HAMMOND, Geoffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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                                            1165 AAATCATCAACAAGT 1179
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102..1253
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36..101
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                       573 AAATCATCAACAAGT 587
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                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                     US-07-829-954-1/c
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LOCATION:
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LOCATION:
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                                                                                                                      RESULT 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                  95563/PS36321/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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; Patent No. 6159469
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REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB340
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ 1D NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULLS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 9556;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
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Matches 15; Conservative
                                                                                                             TELEPHONE: 202-601
                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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                                                                                                                                                                                                                                            single
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                             TOPOLOGY: linear // MOLECULE TYPE: CDNA US-08-452-071-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 ... CITY: ROCKVIlle
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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US-08-961-083-157
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Patent No. 5885820
GENERAL INFORMATION:
APPLICANT: CHANG YIE-HWA
ITILE OF INVENTION: CLONE OF A NUCLEOTIDE SEQUENCE ENCODING
TITLE OF INVENTION: A PROTEIN HAVING TWO FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0%; Score 15; DB 1; Length 1423; 100.0%; Pred. No. 3.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,891
                                                                                                                                                                                                                                                                                                                                                                                                                16777/197/ALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: HOWELL & HAFERKAMP, L.C. 7733 FORSYTH BLVD., SUITE 1400
                                ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                             14-APR-1995
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/994,423
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                            COMPUTER READABLE FORM and with which will made the transfer of the compatible operating system: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                              29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 1423 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
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102..1253
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
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                                                                                                            20007-5109
                                                                                                                                                                                                                                                               FILING DATE: 14
CLASSIFICATION:
                                                                                          USA
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
US-08-421-891-1
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APPLICANT: HAMMOND, Geoffrey L.
APPLICANT: AVVAKNOV, George V.
TITLE OF INVENTION: Variants of Corticosteroid Binding
TITLE OF INVENTION: Globulin
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HAMMOND, Geoffrey L.
APPLICANT: AVAKUMOV, George V.
TITLE OF INVENTION: Variants of Corticosteroid Binding
TITLE OF INVENTION: Globulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/994,423 FILING DATE: 16-DEC-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                            Sequence 1, Application US/07994423 Patent No. 5432080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08421891
Patent No. 5595969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELER: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1423 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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102..1253
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Matches 15; Conservative
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                  412 GTCATTTCTAAGCTG 398
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linear
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LOCATION:
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US-07-994-423-1
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Gaps

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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
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US-09-444-053-3/C
Sequence 3, Application US/09444053A
Sequence 3, Application US/09444053A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lox M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
FILE REFERENCE: RTS-01.2
CURRENT APPLICATION NUMBER: US/09/444,053A
CURRENT FILING DATE: 1999-11-19
SEQ ID NOS: 89
SEQ ID NOS: 89
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             16153-4639
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                                                                APPLICATION NUMBER: US/09/040,799
FILING DATE: 18-MAR-1998
CLASSIFICATION: 536
                                                                                      FILING DATE: 18-MAR-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R
REGISTRATION NUMBER: 35,197
REFRENCE/DOCKET NUMBER: 16153
FELECOMMUNICATION INFORMATION:
TELEFAX: 314-727-5188
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               630 CCCTGCTGCAGAGG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 CCCTGCTGCAGAAGG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 GTTCTTCACGAGGGA 328
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US-09-444-053-3
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                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA US-09-040-799-2
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August 6, 2002, 16:42:48; Search time 19:11 Seconds (without alignments) 1252.027 Million cell updates/sec
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249
1 MLQLWKLVLLCGVLTGTSES.....NVIQQVVDNPQHKTQLQTLI 249
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                               283138 seqs, 96089334 residues
                                                                       OM protein - protein search, using sw model
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pir3:*
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6	0 6	10	32	33	. 34	35	36	37	38	39	40	4.1	42	43	44	45	46	47	48	49	. 20	53	52	53	54	55	26	57	28	59	09	61	62	63	64	65	99	67	89	69	20	. 71	72	73	74	75	

## ALIGNMENTS

RESULT

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hypothetical protein SPBC18H10.11c - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Dacession: T3979
R.Cyne, M.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
R.Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
R.Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
A.Reference number: 221879
A.Rofession: T39775
A.Rotatus: preliminary; translated from GB/EMBL/DDBJ
A.Rotatus: preliminary; translated from GB/EMBL/DDBJ
A.Rotatus: preliminary; translated from GB/EMBL/DDBJ
A.Rotatus: Ball. AL022304; PIDN:CAA18408.1; GSPDB:GN00067; SPDB:SPBC18H10.11c
A.Rotatus acurce: strain 972h-; cosmid c18H10
A.Cross-references: EMBL.AL022304; PIDN:CAA18408.1; GSPDB:GN00067; SPDB:SPBC18H10.11c
A.Rotatus acurce: strain 972h-; cosmid c18H10
A.Gonetics:
A.Map position: 2
C.Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC18H10.11c
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3.2%; Score 8; DB 2; Length 432;

Query Match

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Axcession: B60810
A;Molecule type: protein
A;Malstein, C.
B;Milstein, C.P.; Milstein, C.
B;Dochem, J. 109, 93-99, 1968
B;Title: A tryptic peptide containing a unique serine phosphate residue in rabbit pho
A;Title: A tryptic peptide containing a unique serine phosphate residue in rabbit pho
A;Contents: annotation; active site
C;Comment: This enzyme interconverts glucose-1-phosphate and glucose-6-phosphate, par
C;Comment: This protein is a major substrate for Ca++/calmodulin-dependent protein ki
C;Superfamily; phosphoglucomtase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKEYWORDS: alternative splicing: intramolecular transferase; isomerase; magnesium; m F:2-562 Product; phosphoglucomtuse !, short splice form status experimental CMAT> F:17/Active site: Ser (phosphoserine intermediate) status experimental F:185/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) stat F:408/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) stat F:460/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) stat F:467/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) stat
                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 2-562 <RAY>
R;Yuen, S.; Hunkapiller, M.W.; Wilson, K.J.; Yuan, P.M.
R;Yuen, Blochem. 168, 5-15, 1988
A;Title: Applications of tandem migrobore liquid chromatography and sodium dodecyl su A;Reference number: A60810; MUID:88207910
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A; Experimental source: skeletal muscle
A;Note: authors translated the codon GAG for residue 436 as Gln and CAG for residue
A;Note: these authors refer to this form as isoform 2 or PGM2
A;Note: these authors refer to this form as isoform, 2 or PGM2
J. Biol. Chem. 258, 9166-9174, 1983 uvathingal, J.M.; Mahoney, W.C.
A;Title: The complete amino acid sequence of rabbit muscle phosphoylucomutase.
A;Reference number: A92435; MUID:83265705
A;Reference number: A92435; MUID:83265705
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R.Rivera, A.A.: Eltun, T.S.; Dey, N.B.; Bounelis, P.; Marchase, R.B.
Rene 133, 261-266, 1993
A.Title: Isolation and expression of a rat liver cDNA encoding phosphoglucomutase. A.Reference number: JC2011; MUID:94040821
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F.117/Active site: Ser (phosphoserine intermediate) *status predicted
F.185/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) +
F.460/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) +
F.467/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) +
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 02-Jun-1994 #text_change 18-Jun-1999
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A;Cross-references: GB:L11694; NiD:g393212; PIDN:AAA16862.1; PID:g393213
A;Cross-references: GB:L11694; NiD:g393212; PIDN:AAA16862.1; PID:g393213
A;Experimental source: liver
A;Note: the authors translated the codon GAC for residue 62 as Cys
C;Comment: This enzyme interconverts glucose-1-phosphate and glucose-6-ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%; Score 8; DB 1; Length 562;
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ive 0; Mismatches
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100.0%; Pred. No.
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Best Local Similarity
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 LKVDLGVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross-references: GB:M83088, NID:g189925; PIDN:AAA60080.1; PID:g189926
A.Cross-references: GB:M83088, NID:g189925; PIDN:AAA60080.1; PID:g189926
A.Note: sequence extracted from NCBI backbone (WCBIN:75120, NCBIP:7521)
C.Comment: This enzyme interconverts glucose-1-phosphate and glucose-6-phosphate, partic cromment: This protein is a major substrate for Ca++/calmodulin-dependent protein kinas G.Genetics:
A.Genetics: A.S. Highly polymorphic
A.A.Note: Ious is a highly polymorphic
A.Note: Ious is a highly polymorphic
C.Superfamily: phosphoglucomutase
C.Keywords: intramolocular transferase; isomerase: magnesium; monomer; phosphoprotein; a F.136.7/Aroduct: phosphoglucomutase I %status predicted
F.137.7/Active site: phosphose (Ser) (covalent) (by calmodulin-dependent kinase) #status F.460/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status F.467/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status F.467/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
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C.Species: O.Species: D.S. Putt, W.; Lovegrove, J.U.; Morrison, K.; Hollyoake, M.; Fox, M.F.; H
Proc. Natl. Acad. Sci. U.S.A. 89, 411-415, 1992
A.Title: Phosphoglucomutase I: complete human and rabbit mRNA sequences and direct mappi
A.Reference number: A41801; MUID:92108065
A.Accession: B41801
A.Molecule type: mRNA
A.Residues: 1-562 <WHI>
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J. Biol. Chem. 267, 21080-21088, 1992
Affilte: Purification, characterization, and molecular cloning of a 60-kDa phosphoprotei
A: Reference number: A45077; MUID:93016027
A; Accession: B45077
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A;Cross-references: GB:M97664; NID:9165663; PIDN:AAA31454.1; PID:9165664
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        Pred. No. 10;
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    100.0%;
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                                                       Conservative
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A; Residues: 1-562 <WHL>
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mes 8; Conserv
        Best Local Similarity
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                                                                                                                                208 VSSLLQKE 215
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                                                                                                                                                                                                             84 VSSLLOKE 91
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Gaps

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0; Mismatches

8; Conservative

Matches

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Glycogen phosphorylase (EC 2.4.1.1) [similarity] - Vibrio cholerae (strain N16961 ser) ClSpecies: Vibrio cholerae (5 Jac. 1970 cholerae) d. 18. Aug. 2000 #sequence_revision 20-Aug. 2000 #text_change 24-Aug. 2001 C. Accession: Ag. 1971 M.D.; Dodson, R. C. Clayton, R.A.; Gwinn, M.L.; Dodson, R. C. Hardelberg, J.F.; Eisen, J.A.; Neatherwan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller: I. R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MulD:20406833
A. Accession: A82511
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1 B17 chRis
A. Residues: 1 B17 chRis
A. Residues: 1 B17 chRis
A. Experimental source: Serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                        R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller; J. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methyl-accepting chemotaxis protein VC1859 [imported] - Vibrio cholerae (strain N169)
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C:Superfamily: phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phospl
F:664/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                             C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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Pred. No. 16;
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Matches 8; Conservative 0; Mismatches
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100.0%; Pred. No. 18;
iive 0; Mismatches
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A: Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A: Molecule type: DNA
                                                                                                                                                                                                                                       C; Accession: F82148
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C.Date: 17-Feb-1994 #sequence_revision 02-Jun-1994 #text_change 18-Jun-1999
C.Species: Oryctolagus cuntculus (domestic rabbit)
C.Date: 17-Feb-1994 #sequence_revision 02-Jun-1994 #text_change 18-Jun-1999
C.Accession: A45077
B.Lee, Y.S.: Marks, A.R.; Cureckas, N.: Lacro, R.: Nadal-Ginard, B.; Kim, D.H.
B.Lee, Y.S.: Marks, A.R.; Cureckas, N.: Lacro, R.: Nadal-Ginard, B.; Kim, D.H.
A.Rice Communication of A5077; MUID:93016027
A.Molecule type: mRNA
A.Residues: 1-566 CLES
A.Molecule type: mRNA
A.Residues: 1-666 C.Molecule type: masterial predicted C.Supertainly: phosphoglucomutase 1. long splice form #status predicted
F.12/Active site: Ser (phosphogerine intermediate) #status predicted
F.12/Active site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status
F.41/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
F.47/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
F.47/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
F.47/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
F.47/Pinding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
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C;Species: Caenorhabdiis elegans
C;Species: Caenorhabdiis elegans
C;Species: Caenorhabdiis elegans
C;Date: 15-Oct-1999 #scquence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20875
R;White, S.
R;White, 
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100.0%; Pred. No. 13;
Live 0; Mismatches
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Matches 8; Conservative
                                               163 LKVDLGVL 170
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58 LKVDLGVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 EAEKLLNN 292
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C;Superfamily: H+-transporting ATP synthase chain I
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; transmembrane p
F;12-163/Product: H+-transporting ATP synthase chain b #status experimental <MAT>
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001

A.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MuID:21595285; PMID:11759840
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CiDate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 14-bec-2001
CiPacession: 501399
Riohta, S.; Yohda, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.; Biochim. Biophys. Acta 933-141-155, 1988
A:Title: Sequence and over-expression of subunits of adenosine triphosphate synthase A:Reference number: 501397; MUID:88163679
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A;Cross-references: GB:BA000019; PIDN:BAB75352.1; PID:917132786; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Spēcies: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. cc.
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                                                                                                                                                    Query Match
Best Local Similarity 100...
7; Conservative
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Best Local Similarity 100.0
Matches 7; Conservative
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C;Superfamily: phycocyanin
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                                                                                                                                                                                                                                                                                                178 PTS1SLS 184
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A;Start codon: GTG
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                                                                                                 A; Gene: PH1841
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: Ab1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 3
C;Superfamily: S-receptor Kinase; protein kinase homology; S-locus-specific glycoprotein
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A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137
A;Accession: C71196
      C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000 C;Accession: ¶49010 F;C;Accession: ¶49010 M: Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence batabase, May 2000
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A;Residues: 1-58 «KUPS
A;Cross-references: GB:BAQ00019; PIDN:BAB74082.1; PID:917131475; GSPDH:GN00179
A;Experimental source: strain PCC 7120
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A; Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30962.1; PID:g3258279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein as12383 [imported] - Anabaena sp. (strain PCC 7120) (Sipecies: Anabaena sp. (strain PCC 7120) A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
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C;Date: 14-Aug-1998 #Sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                             Experimental source: cultivar Columbia; BAC clone F25L23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%; Score 8; DB 2 ilarity 100.0%; Pred. No. 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                         Reference number: 225012
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Best Local Similarity
7; Conserva
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                 A; Accession: T49010
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-895 < CDAN>
                                                                                                                                                                                                                                                                                                                                                   A;Gene: ATSP:F25L23.280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AQEAEKL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AQEAEKL 25
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C; Genetics:
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Accession: Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Accession: AB2684
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wockerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC1: Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Atthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan S;Et, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AB2684
A;Status: preliminary
A;Residues: 1-206 < KUR>
A;Cross-references: GB:Ab0008688; PIDN:AAL41888.1; PID:g17739251; GSPDB:GN00186
C;Genetics
A;Genetics
A;Genetics
A;Genetics
A;Map position: circular chromosome
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                                       R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldn
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
                                                                                                                                                                                           A.Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A.Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A.Accession: H97465
A.Scaus: Preliminary
A.Molecule type: DNA
A.Residues: 1-206 < KUR>
A.Cross-references: GB:AE007869; PIDN:AAK86681.1; PID:g15155865; GSPDB:GN00169
G.Genetics:
A.Gene: AGR_C_1598
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100.0%; Pred. No. 54;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches
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Matches 7; Conservative
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C; Accession: H97465
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H97465
hypothetical protein AGR_C_1598 [imported] · Agrobacterium tumefaciens (strain C58, Cere C: Species: Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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Nature 413, 848-852, 2001
A.Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.Authors: preliminary
A.Accession: AH0877
A.Accession: AH
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                                                                                                                                                                                                                                                                                                                                                         Pypothetical protein - Cyanophora paradoxa cyanelle Cipecies: cyanelle Cyanophora paradoxa Cipecies: cyanelle Cyanophora paradoxa Cipecies: cyanelle Cyanophora paradoxa Cipace; 30-Apr-1999 #text_chiange 08-Oct-1999 CiAccession: T06962 Ristiewalt, V.L., Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A. A.Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa. A.Reference number: 215840 A.Accession: T06662 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Accession: T06662 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Roleoule type: DNA A.Residues: 1-179 cSTJ. A.Residues: 1-179 cSTJ. A.Residues: EMBL:030821; NID:g1016083; PIDN:AAA81305.1; PID:g1016218 A.Cross-references: EMBL:030821; NID:glonelm LB555 G.Genome: cyanelle
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches
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Local Similarity 100.0%; Pred. No. 49;
Nes 7; Conservative 0; Mismatches
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79 QEAEKLL 85
                                                                                                      67 QEAEKLL 73
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hypothetical protein yqgE [imported] - Escherichia coli (strain 0157:H7, substrain ED C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: 055952 R;Perna, N T.; Plunkett 111, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wood erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl. Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Stathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: GB.AE005174; NID:g12517494; PIDN:AAG58079.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
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AyTille: The Genome of the Natural Cenetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PWID:11743193
A;Accession: AG2785
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A;Residues: 1-213 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42701.1; PID:917740137; GSPDB:GN00186
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C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C.Accession: AG2785
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Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches
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2.8%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 55;
Best Acthes 7; Conservative 0; Mismatches
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C;Superfamily: hypothetical protein H10304
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74 GILEKLK 80
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                            74 GILEKLK 80
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(Species: Escherichia coli
C;Species: Bcop-1999 | sequence_revision 10-Sep-1999 | text_change 21-Jul-2000
C;Accession: C65080
C;Accession: C65080
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
S;Ence 277, 1453-1462, 1997
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R. Hayashi, T.; Makino, K.; Ohnishi, M.; Kurckawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A.Tille: Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genc A. Accession: H91106
A. Status: preliminary
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A; Residues: 1-211 <BLAT>
A; Residues: 1-211 <BLAT>
A; Cross-references: GBAE000377; GB:U00096; NID:92367178; PIDN:AAC75985.1; PID:91789317;
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: hypothetical protein H10304
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C;Species: Escherichia coli
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A;Residues: 1-211 <4H2
A;Cross-references: GB:BAQ00007; PIDN:BAB37247.1; PID:g13363296; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches
                     A,Cross-references: GB:AP000398; GSPDB:GN00144
A,Experimental source: strain APS
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A,Gene: ECs3824
C;Superfamily: hypothetical protein HI0304
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Best Local Similarity 100.v
Free 7; Conservative
                                                                                                             A;Gene: ribD2; BU462
C;Keywords: oxidoreductase
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Best Local Similarity
7; Conserva
A; Residues: 1-207 <STO>
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Conserved hypothetical protein CP1089 [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Sate: 31 Mar-2000 fsequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: AB1504
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hich
C.; Dodson, R.; Gvinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzh
Nucleic Acids Res. 28, 1397-1406, 2000
A;Fille: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR:
A;Reference number: A81500; MUID:20150255
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A;Cross-references: GB:AE002265; GB:AE002161; NID:97189999; PIDN:AAF38860.1; PID:973
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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Reference number: B72037
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A;Cross-references: GB:AE001437; PIDN:AAK80523.1; PID:g15025597; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC574
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100.0%; Pred. No. 66;
ative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0,,
Matches 7; Conservative 0; Mismatches
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A;Gene: CP1089
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-262 <ARN>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 EAEKLLN 164
                                                                                                                                                                                                                                                                                                                                                                                         80 EAEKLLN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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J. Biol. Chem. 267, 2679-2687, 1992
A;Title: Neonatal rat submandibular gland protein SMG-A and parotid secretory protein ar
A;Reference number: A42337; MUID:92129360
A;Accession: B42337
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J. Bacteriol. 183, 4823-4838, 2001 A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Reference number: A96900; MUID:21359325 A; Reference number: A96900; MUID:21359325 A; Reference number: A96900; MUID:213
   C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: A97565 R;Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liuu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                      A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
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A;Cross-references: GB:AE007869; PIDN:AAK87474.1; PID:g15156796; GSPDB:GNU0169
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Aug-1999
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A;Cross-references: GB:M83209; NID:g206456; PIDN:AAC06334.1; PID:g206457
A;Cross-reference extracted from NCBI backbone (NCBIN:78709, NCBIP:78710)
C;Genetics:
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Best Local Similarity 100.0%; Pred. No. Jo.
Matches 7; Conservative 0; Mismatches
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A:Map position: circular chromosome
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Best Local Similarity Tove.
Tr Conservative
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Best Local Similarity 100...
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Matches 7; Conservative
                            A; Molecule type: DNA
A; Residues: 1-270 <PAR>
A; Status: preliminary
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                                                                          CT598 hypothetical protein (imported) - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: E86588
R;Shirai, M.: Hirakawa, H.: Kimoto, M.: Tabuchi, M.: Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: ABOS02; PMID:11677608
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C;Genetics:
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C.Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 29-Oct-1999
C;Accession: S48317
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Superfamily: Saccharomyces hypothetical protein YFL013w-a
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C,Genetics:
A,Gene: CPj0783
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Best Local Similarity
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A; Residues: 1-267 <CHU>
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A; Residues: 1-262 <ST0>
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A;Map position: 6L
C;Superfamily: Sacchard
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probable DNA binding protein [imported] - Escherichia coli (strain O157:H7, substrain Cispecies: Escherichia coli (cispecies: Escherichia coli (cispecies: Escherichia coli (strain O157:H7, substrain Cispecies: Escherichia coli (strain O157:H7, substrain Cispecies: Escherichia coli O157:H7, substrain 1996586 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Casavara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B. 11-22, 2001 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and casavarance number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: G64726
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-271 <BLAT>
A;Cross-references: GB:AE000116; GB:U000966; NID:q1786240; PIDN:AAC73166.1; PID:g1786:
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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A;Cross-references: GB:AL513382; PIDN:CAD01250.1; PID:g16501379; GSPDB:GN00176
C;Genetics:
A;Gene: dj!A
C;Superfamiliy: dnaJ amino-terminal homology
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A;Status: prefilminary
A;Molecule type: DNA
A;Residues: 1-271 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33483.1; PID:g13359516; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yabH protein - Escherichia coli
C)Species: Escherichia coli
C)Sate: 12-Sep-1997 *sequence_revision 17-Sep-1997 *text_change 08-0ct-1999
C)Accession: G64726
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C.Superfamily: dnaJ amino-terminal homology
C.Superfamily: transmembrane protein
F:13-29/Domain: transmembrane #status predicted <TMM>
F:205-271/Domain: dnaJ amino-terminal homology <DNJ>
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Live 0; Mismatches
                                                                                                                                                                                      2.8%; Score 7; 1
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8%; Score 7;
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Nable dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - land snail mitochondrion Nable dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - land snail mitochondrion C. Species: mitochondrion Albinaria coerulea (land snail)
C. Species: mitochondrion Albinaria coerulea (land snail)
C. Species: mitochondrion Albinaria coerulea (land snail)
C. Species: mitochondrion G. C. Lecanidou, R. R. Hext_change 24-Oct-2000
C. Accession: 559153
A. Title: Complete sequence and gene organization of the mitochondrial genome of the J. A. Recession: 559143; MUID:96120351
A. Accession: 559153
A. Status: translation not shown
A. Molecule type: DNA
A. Residues: 1-307 < HAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cipecies: Rhodobacter capsulatus
Cipecies: Cipecies: Cipecies: V.: Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
R;Vicek, C.; Paces, V.: Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB: A;Reference number: 214955, MuID:97404404
A;Reference number: 214955, MuID:97404404
A;Astatus: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: Laso cv.C.>
A;Cross-references: EMBL:AF010496; NID:93128256; PIDN:AACI6211.1; PID:93128359
C;Genetics: Coss-references: EMBL:AF010496; NID:93128256; PIDN:AACI6211.1; PID:93128359
                             Organization in 2000 - Cardinabults elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15.0ct-1999 #sequence_revision 15.0ct-1999 #text_change 18-Feb-2000
C.Date: 15.0ct-1999 #sequence_revision 15.0ct-1999 #text_change 18-Feb-2000
C.Date: 15.0ct-1999 #sequence_revision 15.0ct-1999 #text_change 18-Feb-2000
R.Matchews, L.
Submitted to the EMBL Data Library, March 1996
A.Reference number: 220406
A.Reference number: 220406
A.Reference number: 220406
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-290 <a href="https://doi.org/10.00028/">Molecule type://doi.org/10.00028/</a>, Tessp: ZK1086.3
A.Map position: X
A:Introns: 85/3: 110/1: 125/3: 165/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 7; DB 2; Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribose transport ATP-binding protein - Rhodobacter capsulatus
         hypothetical protein 2K1086.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 77; tive 0; Mismatches
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Matches 7; Conserval
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|142 ||LEKLKV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 LILDVKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 LILDVKA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 ILEKLKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AF0061
DnaJ-like protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0061
C;Genetics: Af0061
C;Accession: AF0061
C;Genetics: Af0061
C;CyCorrection: AF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable DNA binding protein yabH [imported] - Escherichia coli (strain 0157:H7, substra
C:Species: Escherichia coli
C:Species: L6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85487
R:Perna, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
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    DB 2; Length 271;
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                                                                                             0; Indels
2.8%; Score 7; DB 2;
100.0%; Pred. No. 69;
tive 0; Mismatches
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100.0%; Pred. No. 69;
tive 0; Mismatches
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Best Local Similarity 100.00
Free 7; Conservative
Query Match 2.8%
Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                                                                                                                 74 AKQKAQE 80
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C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nv-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1883
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.
F; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Ritle: Comparative genomics of Listeria species.
A;Ritle: Comparative genomics of Listeria species.
A;Ritle: Cumber: AB1077; MUID:21537279; PMID:11679669
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A:Note: Anabaena sp.
A:Note: Anabaena sp.
A:Note: Anabaena sp.
A:Note: Anabaena sp.
C.Date: Jule Co. 2001
A:Note: Machaena sp.
C.Date: Jule Co. 2001
C.Date: Jule Co. 2001
C.Date: Jule Co. 2001
C.Date: Jule Co. 2001
C.Date: Jule C. 2001
C.Date: Jule Co. 2001
C.Da
                                                        A;Cross-references: GB:299121; GB:AL009126; NID:92635827; PIDN:CAB15427.1; PID:926359
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein Imo2472 [imported] - Listeria monocytogenes (strain EG
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A;Cross-references: GB:NC_003210; PIDN:CAD00550.1; PID:916411960; GSPDB:GN00177
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C:Superfamily: Streptomyces coeliculor hypothetical protein SCC54.10c
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100.0%; Pred. No. 81;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 7; 1
100.0%; Pred. No.
                                                                                                                                                                                                    C)Genetics:
A;Gene: yvff
C;Superfamily: hypothetical protein yxaB
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Best Local Similarity 100.0
7, Conservative
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Best Local Similarity 100.0
Matches 7; Conservative
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C;Superfamily: phoW protein
              A; Residues: 1-322 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 SSLLQKE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GLKISNS 107
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Andriacies: Bacillus subliss
Andriacies: Bacillus subliss
Cipacies: A: Galizzi, A: Galizzi
Andriacies: Cipacies: A: Galizzi, A: Galizzi, A: Galizzi
Andriacies: Cipacies: A: Lapidus, A: Canlonis, A: Authors: Labidus, A: Contacter, B: Roche, B: Rose, M: Sadaie, Y: Sato, T: Scanlon, A: Authors: Schleich, S: Schroeter, R: Scocifone, F: Sekiguchi, J: Sekwaka, A: Seron akeuchi, M: Tamakoshi, A: Tamaka, T: Tampara, T: Topponi, A: Topato, V: Yoshida, R: A: Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A: Accession: G70037
A: Status: pretiminary: nucleic acid sequence not shown; Lranslation not shown
A:Cross-references: EMBJ.:X83390; NID:9975668; PIDN:CAA58306.1; PID:9975679; GSPDB:GN0013
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Anabaena sp.
Anote: Anabaena sp.
Anote: Anabaena sp.
Cispecies: Anabaena sp.
Cistrain PCC 7120) is a synonym of Nostco sp. strain PCC 7120
Cistrain PCC-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
Cistrain AE2384
FX and ANOTE: Anabaena and Anote and
                                                                                                                                     A:Genome: mitochondrion
A:Genetic code: SGC4
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: membrane-associated complex; mitochondrion; NAD: oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Pred. No. 79;
Live 0; Mismatches 0; Indels
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les 7; Conservative
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Best Local Similarity
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218 SISLSLL 224
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ArTitle: Evidence for lateral gene transfer between Archaea and Bacteria from genome A. Reference number: A72200; MUD: 99287316
A. Reference number: A72200; MUD: 99287316
A. Status: preliminary
A. Mosedule type: DNA
A. Residues: 1-383 < ARN
A. Cross-references: GB. AE001737; GB. AE000512; NID: 94981144; PIDN: AAD35709.1; PID: 949.
A. Experimental source: strain MSH8
A. Gene: TM0625
C. Seperfamily: Thermotoga maritima hypothetical protein TM0625
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C;Species: Bacillus halodurans
C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D84068
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; I
                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Gen. Genet. 230, 401-412, 1991
A.Title: Organisation and functions of the actVA region of the actinorhodin biosynthm
A.Reference number: S18539; MUID:92114870
A.Reference numbers S18539; MUID:92114870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                          hypothetical protein 5 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72352
      Gaps
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R,Caballero, J.L.; Martinez, E.; Malpartida, F.; Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 7; DB 2; Length 381; ilarity 100.0%; Pred. No. 94; Conservative 0; Mismatches 0; Indels
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         Indels
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         Mismatches
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Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
      0;
      Conservative
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Best Local Similarity
...ns 7; Conserva
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A;Residues: 1-381 <CAB>
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                                                                                                                  323 LPTNTDI 329
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                                                         93 LPTNTDI 99
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7;
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                                                                                                                                                                                                       RESULT 44
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      Matches
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R; Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A; Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI A; Reference number: Z17775, MUID: 97398704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F95861
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endd A;Reference number: A95842; MUID:21396508; PMID:11481431
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R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
A Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Abalt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weills, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUD:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Atlantic hagfish mitochondrion
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A;Residues: 1-374 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC48558.1; PID:915140030; GSPDB:GN00167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-348 <DEL>
A;Cross-references: EMBL:Y09527; NID:92340019; PIDN:CAA70717.1; PID:92340021
                                                                                                                                                                                                                                                                                                                                                                      C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
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                                 DB 2; Length 343;
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A;Molecule type: DNA
                           2.8%; Score 7; DB 2
100.0%; Pred. No. 85;
tive 0; Mismatches
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Query Match
Best Local Similarity 100...
Best Local 7;. Conservative
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Best Local Similarity
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                                                                                                                                          181 ISLSLLD 187
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                                                                                                                                                                           282 1SLSLLD 288
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R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. gasawara, N.; Yasunaya, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B. 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g A; Reterence number: A99629; MUJD:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-390 <STO>
A;Cross-references: GB:AE005174; NID:g12519339; PIDN:AAG59511.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
                                                                                     isoaspartyl dipeptidase [imported] - Escherichia coli (strain 0157:H7, substrain RIMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoaspartyl dipeptidase [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                         C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Accession: F91289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: C86131 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000
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C;Superfamily: Wacillus dihydroorotase; Bacillus dihydroorotase homology
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C;Superfamily: Bacillus dihydroorotase; Bacillus dihydroorotase homology
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A,Accession: C86131
A,Status: preliminary
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Best Local Similarity
7; Conserva
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A;Molecule type: DNA
A;Residues: 1-390 <HAY>
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Best Local Similarity
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A; Residues: 1-390 cBUR
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete qenome sequence of Escherichia coli K-12.
                                                                                                                                           A;Molecule type: DNA
A;Residues; 1-389 <STO>
A;Cross-references: GB:A#001518; GB:BA000004; NID:g10175792; P1DN:BAB07067.1; GSPDB:GN00
A;Experimental source: strain C-125
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J. Bloi. Chem. 270, 4076-4087, 1995
A.Title: Purification and characterization of an isoaspartyl dipeptidase from Escherichi
A.Reference number: A55889; MUID:95181377
A.Recession: B55889
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MULD:20512582; PMID:11058132 A;Accession: D84068
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R;Burland, V; Plunkett III, G: Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
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C.Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 08-Oct-1999
C.Accession: B55889; S56553; B65247
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ilarity 100.0%; Pred. No. 96;
Conservative 0; Mismatches 0; Indels
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C;Superfamily: translation initiation factor eIF-4A
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Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches
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A; Accession: S56553
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A;Accession: B65247
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Best Local Similarity
7; Conserva
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A; Residues: 1-390 <BLAT>
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P80556 anabaena sp
P4014 bacillus ca
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P57534 buchnera ap
090690 gallus gall
090690 gallus gall
091680 escherichia
P54692 bacillus li
P4802 abcillus li
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P54692 bacillus al
P6405 accharichia
045435 caenorhabdi
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P2259 sacchariomyc
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P38677 rattus norv
Q00963 drosophia
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rattus norv
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249
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Copyright (c) 1993 - 2000 Compugen Ltd.
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DAAA_BACLI
NU2M_ALBCO
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FTS1_ECOLI
PLB1_YEAST
SIN4_YEAST
SIP3_YEAST
SC25_YEAST
GP21_RAT
SP21_RAT
SPCB_DROME
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HAN2_HUMAN
HAN2_MOUSE
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YV4Q_CAEEL
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ATPF_BACP3
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RID2_BUCAI
                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                 PGMU_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                               PHAC_ANASP
                                                                                                                                                                                                                                                               Post-processing: Listing first 75 summaries
                                                                                                                                                                                                                                                                                                                                                                                                           PGMU_RABIT
PGMU_RAT
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TXC9_CUPSA
                                                                                                                                                    Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC (ISOFORM 1).
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- POLYMORPHISM: MANY POLYMORPHIC VARIANTS OF PGMI EXIST. 8 DIFFERENT ALLEES ARE KNOWN: PGMI**1+, PGMI*1-, PGMI*2-+, PGMI**2-+, PGMI**3-, PGMI*7-+, AND PGMI*7--, THE SEQUENCE OF PGMI*1+ IS SHOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate = alpha-D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVKVFQSSANYA -> KTYYFEEKPCYL (IN ISOFORM
                                                                                                                                                                                                                                                                                                      March R.E., Putt W., Hollyoake M., Ives J.H., Lovegrove J.U., popkinson D.A., Edwards Y.H., Whitehouse D.B.;
"The classical human phosphoglucomutase (PGM1) isozyme polymorphism is generated by intragenic recombination.";
Proc. Natl. Acad. Sci. U.S.A. 90:10730-10733(1993).
-!- FUNCTION: THIS ENZYME PARTICIPATES IN BOTH THE BREAKDOWN AND SYNTHESIS OF GIUCOSE.
                                                                                                                                                                                                   "Intragenic recombination at the human phosphoglucomutase 1 locus: predictions fulfilled."; Proc. Natl. Acad. Sci. U.S.A. 90:10725-10729(1993).
            SEQUENCE OF 1-81 FROM N.A. (ISOFORM 1).
BEDLINE-94079685; Pubmed-8257433;
Putt W., Ives J.H., Hollycake M., Hopkinson D.A., Whitehouse D.B.,
Edwards Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMS THE PHOSPHOSERINE INTERMEDIATE (BY SIMILARITY).
VKIVTVKTQAYQ -> EEGPLPLLTFATAPYH (IN
                                                                                  "Phosphoglucomutase 1: a gene with two promoters and a duplicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFORM 2).
FYMKEAIQLIARI -> YFNKSA1ETIVQM (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
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                                                                                                                                                    VARIANTS MET-67; CYS-220 AND HIS-419.
                                                                                                                                                                                                                                                                                     MEDLINE=94068475; PubMed-7902568;
                                                                                                                                                                    MEDLINE=94068474; PubMed=7902567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL109925; CAB92085.1; -. EMBL; AL109925; CAB92086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF02880; PGM_PWM_III; I. PRINTS, PR05099; POMPMM.
PROSITE: PS00710; PGM_PWM: I. Isomerase; Phosphorylation; Mac
                                                                                                                 Biochem. J. 296:417-422(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGM_PMM_I1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001485; PGM_PMM.
                                                                                                                                                                                                                                                                         VARIANTS CYS-220 AND HIS-419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00408; PGM_PMM; 1.
Pfam: PF02878; PGM_PMM_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S67989; AAH29177.2; -.
                                                                                                                                                                                      Takahashi N., Neels J.V.;
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                                                                         /FTId = VAR_006091.
Y -> H (IN PGM1*1-, PGM1*2-, PGM1*3- AND
                              /FTId=VAR_006090.
R -> C (IN PGM1*2+, PGM1*2-, PGM1*3+ AND
 K -> M (IN PGM1*7+, PGM1*7-, PGM1*3+ AND
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification, characterization, and molecular cloning of a 60-kDa phosphoprotein in rabbit skeletal sarcoplasmic reticulum which is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Milstein C.P., Milstein C.; "A tryptic peptide containing a unique serine phosphate residue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ray W.J. Jr., Hermodson M.A., Puvathingal J.M., Mahoney W.C.; "The complete amino acid sequence of rabbit muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee Y.S., Marks A.R., Gureckas N., Lacro R., Nadal-Ginard B.,
                                                                                                                                                                                                 DB 1; Length 561; 0. 4.3;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
NCBI_TaxID=9986;
                                                                                                                                      R -> G (IN REF. 3).
61B7D517EEA9FE4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 89:411-415(1992).
                                                                                                                        /FTId=VAR_006092.
                                                                                                                                                                                                                                                                                                                                                                 PGMU_RABIT STANDARD: PRT; 561 AA. P00944; P38651; 21-JUL-1986 (Rel. 01, Created) 1-JUL-1986 (Rel. 01, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                 pred. No. 4.3
0; Mismatches
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Dai J.B., Liu Y., Ray W.J. Jr., Konno M.;
                                                                                                                                                                                                 3.2%; Score 8;
100.0%; Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoform of phosphoglucomutase.";
J. Biol. Chem. 267:21080-21088(1992).
                                                                                                         PGM1 *7-
                                                            PGM1 *3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 258:9166-9174(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92108065; PubMed=1530890;
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MEDLINE-93016027; PubMed-1328221;
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61318 MW:
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Matches 8; Conserv
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3.2%; Score 8;
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                                                                                                - 1- COFACTOR: KEQUIRES MAGNESIUM FOR ACTIVITY.
- 1- SUBUNT: MONOMER.
- 1- SUBUNT: MONOMER.
- 1- SUBCELLULAR LOCATION.
- 1- SUBCELLULAR LOCATION.
- 1- SUBCELLULAR LOCATION.
- 1- SUBCOPLASMIC RETICULAR SELETAL
SARCOPLASMIC RETICULAR.
- 1- SUBCOPLASMIC RETICULAR.
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- 1- PTW. 1SOFORM 2 IS THE MAJOR CALMODULIN-DEPENDENT PHOSPHOPROTEIN IN
- 1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
- 1- DATABASE: NAME-WORTHINGTON enzyme manual;
                                                            Acta Crystallogr. D 53:392-405(1997).
--- FUNCTION: THIS ENZYME PARTICIPATES IN BOTH THE BREAKDOWN AND SYNTHESIS OF GLUCOSE.
---- CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate - alpha-D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                          RVKVFQSSTNYA -> KTYYFEDKPCYL (IN ISOFORM
The crystal structure of muscle phosphoglucomutase refined at 2.7-A esolution.",
                                                                                                                                                                                                                                                                                                                                                                                                                 FORMS THE PHOSPHOSERINE INTERMEDIATE. VKIVIVKTKAYP -> EEGPLPLLTIRTAPYH (IN
                                       Liu Y., Ray W.J. Jr., Baranidharan S.;
"Structure of rabbit muscle phosphoglucomutase refined at 2.4-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOFORM 2).
FYMKEAIQLIVRI -> YFNKSAIETILQM (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISTVEPAQRQEAT -> FFSIDLKDRQGSS (IN
                                                                                                                                                                                      WWW*"http://www.worthington-biochem.com/manual/P/PGM.html".
                                                                                                                                                                                                                                                                                                                                                                                             Isomerase; PhosphoryLation; Magnesium; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOFORM 2).
                              X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
       resolution.";
J. Biol. Chem. 267:6322-6337(1992).
                                                                                                                                                                                                                                                               EMBL, M97664; AAA31454.1; --
EMBL: M97663; AAA31453.1; --
PIR, A01175; PMRB.
PIR, A45077; PMRB.
PIR, B41801; B41801.
PDB; 3PMG; 07-DEC-95.
PDB; 1DV; 12-MAR-97.
PDB; 1VKL; 11-JAN-97.
InterPro, IPR001485; PGM_PMM. 1
Pfam; PF00408; PGM_PMM. 1
Pfam; PF02878; PGM_PMM. 11.
Pfam; PF02879; PGM_PMM. 11.
PRNINTS; PR005809; PGM_PMM. 11.
PROSITE; PS00710; PGM_PMM. 1
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                                                                                            6-phosphate.
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INIT_MET
ACT_SITE 11
                                                     resolution."
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61427 MW; 6D8AFB26B0242832 CRC64;
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DB 1; Length 561;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate = alpha-D-glucose
                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 133:261-266(1993).
-:- FUNCTION: THIS ENZYME PARTICIPATES IN BOTH THE BREAKDOWN AND
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                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM).
                                                                                                                                                                                                                                                                                                                                                                                                                          Rivera A.A., Elton T.S., Dey N.B., Bounelis P., Marchase R.B., "Isolation and expression of a rat liver cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 8; DB 1; Length 561;
100.0%; Pred. No. 4.3;
tive 0; Mismatches 0; Indels
                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585A151D49170A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
100.0%; Pred. No. 4.3;
iive 0; Mismatches
                                                                                                                                                                      561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PRO0509; PGMPMM.
PROSITE; PSO0710; PGM_PMM; 1.
Isomerase: Phosphorylation; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94040821; Pubmed=8224913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piam; PF00408; PUM PMM: 1.
Pfam; PF02878; PUM PMM_1; 1.
Pfam; PF02879; PUM PMM_11; 1.
Pfam; PF02880; PGM_PMM_111; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 AA; 61272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCM_PMM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L11694; AAA16862.1; -.
 Best Local Similarity 100.0
Matches B; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHESIS OF GLUCOSE
                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00408; PCM_PMM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoglucomutase
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                                                                                162 LKVDLGVL 169
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                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                   53 LKVDLGVL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-phosphate.
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                                                                                                                                                                      PGMU_RAT
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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, ONE ALPHA-B CHAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ducret A., Sidler W., Wehrli E., Frank G., Zuber H.; "Isolation, characterization and electron microscopy analysis of a hemidiscoidal phycobilisome type from the cyanobacterium Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: LIGHT-HARVESTING PHOTÓSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM ABSORPTION AT APPROXIMATELY 654 NANOMETERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00502; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                 Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yanaba M., Sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THREE BETA CHAINS.
-1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                                                                               Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHYLATION (BY SIMILARITY). PHYCOCYANOBILIN CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 7; DB 1; Length 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
6E814C32F2857BD6 CRC64;
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
                                                       (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003593; BAB75352.1; -.
InterPro; IPR001659; Phycobilisome.
                                                                                                                                                                                                                  MEDLINE-21595285; PubMed-11759840;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-28.
MEDLINE-96270757; PubMed-8665889;
                                                                                                                              Anabaena sp. (strain PCC 7120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylation; Completé proteome.
                                  01-FEB-1996 (Rel. 33, Created)
                                                                                       Allophycocyanin alpha-B chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 AA; 17680 MW;
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     STANDARD;
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Best Local Similarity
                                                                                                                                                              NCBI_TaxID=103690;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                        01-MAR-2002 (Rel.
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                                                                                                            APCD OR ALL3653
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01-FEB-1995 (
16-OCT-2001 (
PHAC_ANASP
P80556;
                                                         01-MAR-2002
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P41014;
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 21.2 kDa protein in YCF23-APCF intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
NCBL_TaxID=2762;
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                                                                                                                                                                                                                                                                                        DB 1; Length 163;
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                           163 AA; 18566 MW; BBE790CA0EF18ACF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       il protein; Cyanelle.
179 AA; 21248 MW; 046AF1943F4F57E2 CRC64;
                                                                                                                                                                                     ATP SYNTHASE B CHAIN.
                                                                            PIR, S01399, S01399,
InterPro; IPR002146; ATP-synt_B.
Pfam; PF00430; ATP-synt_B; 1.
Hydrogen ion transport; Transmembrane; CF(0).
                                                                                                                                                                                                                                                                                        Query Match 2.8%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches
                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         POTENTIAL.
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01-FEB-1996 (Rel. 33, Last sequ
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                                                           EMBL; X07804; CAA30650.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                     163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyanophora paradoxa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                         79 QEAEKLL 85
                                                                                                                                                                                                                                                                                                                                                                                                                67 QEAEKLL 73
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SEOUENCE 13
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                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                               SEQUENCE
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European Bioinformatics Institute. There are no restrictions on its
by non-profit institutions as long as its content is in no way
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Submitted (AUC-1994) to the EMBL/GenBank/DDBJ databases.
Submitted (AUC-1994) to the EMBL/GenBank/DDBJ databases.

-!- SUBMIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBMITTS: ALPHA(3), BETPA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBMITS: A, B AND C.
-!- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA; 18588 MW; AC75BF93D031C088 CRC64;
                                                             Firmicutes, Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00430; ATP-synt_B; 1.
Hydrogen ion transport; Transmembrane; CF(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthase B chain precursor (EC 3.6.3.14).
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches
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                                                                                   Bacillus/Staphylococcus group; Bacillus.
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ATP synthase B chain (EC 3.6.3.14).
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                                           Bacillus caldotenax.
                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                    NCBI_TaxID=1395;
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P09221;
                                                                 Bacteria;
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Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Joon K.W., Mueller N.E.,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Núcleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol, Rep. 13:327-332(1995).
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/annource/
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193) (HTP
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.I., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rose C.K., Mayhew G.F.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B., "Enrichment of low abundance proteins of Escherichia coli by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%; Score 7; DB 1; Length 187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 AA; 20686 MW; 8ACCCCACABF4E025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Efectrophoresis 20:2181-2195(1999).
                                                                                                                                               YQGE_ECOLI STANDARD, PRT; 187 AA. PS2049; P76648; 01-0cT-1996 (Rel. 34, Created) 10-0cT-1996 (Rel. 34, Last sequence update) 16-0cT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC75985.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U28377; AAA69115.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydroxyapatite chromatography.
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Best Local Similarity 100.00
7; Conservative
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Pfam; PF02622; DUF179; 1.
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InterPro; IPR003774; DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 187 AA
                                                                                                                                                                                                                                                                                                               Escherichia coli
165 HQPVAVL 171
                                        7 HOPVAVL 13
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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50 GILEKLK 56
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YQGE OR B2948.
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Fernandez-Teran M., Piedra M.E., Kathiriya I.S., Srivastava D.,
Rodriguez-Rey J.C., Ros M.A.;
"Role of dHAND in the anterior-posterior polarization of the limb bud:
                                                                                                                                                                                                                                                                                          Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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"A subclass of bHLH proteins required for cardiac morphogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heart- and neural crest derivatives-expressed protein 2 (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND).
                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002734; RibD_C.
Pfam; PF01872; RibD_C; 1.
Riboflavin biosynthesis; Oxidoreductase; NADP; Complete proteome.
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                           symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA; 23942 MW; DAC973284089D76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last aunotation update)
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. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Embryo;
MEDLINE-96123273; PubMed-8533092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001119; BAB13159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 270:1995-1998(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAND2 OR DHAND.
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C -1- DEVELOPMENTAL STAGE: AT STAGES 8 TO 9, EXPRESSED IN THE WHOLE LATERAL PLATE MESODERM AND PRECARDIGGENIC MESODERM. AT STAGE 10, EXPRESSED THROUGHOUT THE CARDIAC TUBE AND THE SINGS VENDSOS. BY STAGE 15, EXPRESSED HOWOGENOUSLY IN THE VENTIOUS REGION OF THE HEART, INCLUDING THE ATRIA, FUTURE LEFT VENTRICLE, BULBUS CORDIS C AND THE PRESSED THROUGH STAGE 20, BUT DECREASES THEREFIER. IN THE DEVELOPING LIMBS, FROM THE INITIATION OF THE BUDS (STAGES 16 TO 17), EXPRESSION ENCROPED STAGE 20, BUT DECREASES THEREFTER. IN SUDS SO THAT A GRADIENT EXPRESSION ALONG THE ANTERIOR OF THE LIMB BUDS SO THAT A GRADIENT EXPRESSION ALONG THE ANTERIOR POSTERIOR AXIS OF THE BUD IS ESTABLISHED WITH HIGHER EXPRESSION AT THE POSTERIOR BOYDER. AT LATER STAGES, EXPRESSION AT THE POSTERIOR BOYDER. AT LATER STAGES, EXPRESSION OF RECORDS IN THE AUTOPOD, DYNAMIC EXPRESSION OF HAND TO THE POSTERIOR AUTHERDIGITAL.

THE AUTOPOD, DYNAMIC EXPRESSION OF HANDS AFFECTS THE INTERDIGITAL PREVIOUSLY. THE LATERAL BORDERS OF THE DIGITS AND EVENTUALLY THE DEVENTORING VERWINDS AFFECTS THE INTERDIGITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPING VENTRAL TENDONS.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                 Development 127:2133-2142(2000).
-!- FUNCTION: ESSENTIAL FOR CARDIAC MORPHOGENESIS. BINDS DNA ON E-BOX CONSENSUS SEQUENCE 5'-CANNTG-3' (BY SIMILARITY). PLAYS AN
                                                                                                                                 .i. SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
                                                               CONSENSUS SEQUENCE 5'-CANNTG-3' (BY SIMILARITY). PLAYS AN IMPORTANT ROLE IN LIMB DEVELOPMENT, PARTICULARLY IN THE ESTABLISHMENT OF ANTERIOR-POSTERIOR POLARIZATION OF THE LIMB BUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAND HAND STANDARD; PRT; 217 AA. 095301; P97833; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Heart- and neural crest derivatives expressed protein 2 (Deciduum, expressed protein 2) (dHAND). HAND2 OR DHAND.
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Developmental protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 7; DB 1; Length 216; 100.0%; Pred. No. 19; tive 0; Mismatches 0; Indels
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HELIX-LOOP-HELIX MOTIF.
0B3F052F2CC34C6B CRC64;
implications for the Sonic hedgehog pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ARG
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98 110 BA
111 154 HE
216 AA; 24407 MW;
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InterPro, IPR001092; HLH_dim.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00353; HLH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P10085; 1MDY
                                                                                                                                                      BHLH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 LKSTVSS 210
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DOMAIN
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HAN2_HUMAN
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**REMIP P., GTAINGET D., METCALES J.;

**EXPRESSION of helix-loop-helix proteins in vascular smooth muscle.*;

**EXPRESSION of helix-loop-helix proteins in vascular smooth muscle.*;

**LEXPRESSION of helix-loop-helix proteins in vascular smooth muscle.*;

**LEXPRESSION OF THE RIGHT VENTRICLE AND OF THE AORTIC LARLY FOR THE FORMATION OF THE RIGHT VENTRICLE AND OF THE AORTIC ARCIOCARLY FOR VASCULAR DEVELOPMENT AND REGULATION OF AND OFFICE AND OF THE AORTIC PROTEIN AND REGULATION OF AND OFFICE AND OFFICE AND OFFICE AND OFFICE ESTABLISHMENT OF ANTERIOR POSTERIOR POLARIZATION, ACTING AS AN OFFICE AND OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- TISSUE SPECIFICITY: HEART.
-:- DEVELOPMENTAL STAGE: EXPRESSED IN THE FETAL HEART.
-:- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Developmental protein; Angiogenesis; Transcription regulation;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 217;
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HELIX-LOOP-HELIX MOTIF.
; 528F541BB2173F1E CRC64;
                                                                                                                                                 Russell M.W., Kemp P., Wang L., Brody L.C., Izumo S.; "Molecular cloning of the human HAND2 gene."; Biochim. Biophys. Acta 1443:393-399(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AA
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. SPECIES=Rat; STRAIN=WISTAR; TISSUE=Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; |
Pred. No.
                                                                                                  SPECIES-Human; TISSUE-Embryonic heart; MEDLINE-99096473; Pubmed-9878849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY - ALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF087940; AAD13185.1; -. EMBL; AF087941; AAD13186.1; -.
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217 AA; 23666 MW;
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InterPro; IPR001092; HLH_dim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y08138; CAA69332.1; -. HSSP; P10085; 1MDY.
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Best Local Similarity
7; Conserva
                                                                      SEQUENCE FROM N.A.
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Q61039; Q61100;
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ID HAN2_MO
AC Q610399
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"A signaling cascade involving endothelin-1, dHAND and msxl regulates development of neural-crest-derived branchial arch mesenchyme."; Development 125:3005-3014(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firulli B.A., Hadzic D.B., McDaid J.R., Firulli A.B., "The basic helix-loop-helix transcription factors dHAND and eHAND exhibit dimerization characteristics that suggest complex regulation
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
Heart and neural crest derivatives-expressed protein 2 (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND) (Helix-loop-helix transcription factor expressed in embryo and deciduum) (Thing-2).
                                                                                                                                                                                                                                                        Srivastava D., Cserjesi P., Olson E.N.; "A subclass of bHLH proteins required for cardiac morphogenesis.";
                                                                                                                                                  Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090:
                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                           Cross J.C., Flannery M.L., Blanar M.A., Steingrimsson E., Jenkins N.A., Copeland N.G., Rutter W.J., Werb Z.; "Hxt encodes a basic helix-loop-helix transcription factor that regulates trophoblast cell development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charite J., McFadden D.G., Olson E.N.; "The bHLH transcription factor dHAND controls Sonic hedgehog expression and establishment of the zone of polarizing activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98337821; PubMed=9671575;
Thomas T., Kurihara H., Yamagishi H., Kurihara Y., Yazaki Y.,
Olson E.N., Srivastava D.;
                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SV; TISSUE=Embryoid bodies; MEDLINE=95401868; PubMed=7671815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bHLH transcription factor, dHAND.";
Nat. Genet. 16:154-160(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION, AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION, AND DEVELOPMENTAL STAGE.
MEDLINE-20265920; Pubmed-10804186;
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                                                                                                                                                                                                                                       MEDLINE=96123273; PubMed-8533092;
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                                                                                                             HANDS OR DHAND OR HED OR THINGS.
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                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 92-203 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during limb development.
                                                                                                                                (Mouse)
                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                           TISSUE-Embryo;
                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of function.
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ARCH ARTERIES, AND IN PHARTYGEAL ARCHES, AS THE HEART LOOPS, THE EXPRESSION BECONES RESTRICTED TO THE CONOTRUNCUS AND FUTURE RIGHT VENTRILE (ENDOCARDIUM). AT 10.5 DPC, HIGHLY VENTRICLE (ENDOCARDIUM), AT 10.5 DPC, HIGHLY EXPRESSED IN THE BRANCHIAL ARCHES, AS WELL AS IN THE TRUNCUS ARTERIOSUS, AORTIC SAC, AND THE VASCULAR MESENCHYME BETWEEN THE THIRD AND FOUNTH AORTIC ARCH ARTERIES, WHICH LATER GIVES RISE TO VASCULAR SWOOTH MUSCLE CELLS AND TO THE MESENCHYME OF THE PHARTYNGEAL ARCH ON DAY 13.5 PC, BARELY DETCTABLE IN THE HEART, BUT APPARENT IN THE NEURAL SIMILAR TO THAT OF HANDI. IN THE DEVELOPING LIMES, EXPRESSION IS DETECTED IN THE POSTERIOR MESODERM OF THE BUOSA AT 9.5 DPC. IT IS THEN PROGRESSIVELY DOWN-REGULARD AT THE ANTERIOR OF THE LIME BUOSS OF THE BUDS SO THE LIME BUDS SO FLIME EXPRESSION ALONG THE ANTERIOR OF THE LIME BUDS SO THE BUD IS ESTABLISHED WITH HIGHER EXPRESSION AT THE POSTERIOR BUDS SO THE BUD IS ESTABLISHED WITH HIGHER EXPRESSION AT THE POSTERIOR BUDGOD. IN THE AUTOPOD, DYNAMIC EXPRESSION AT THE POSTERIOR AND TO THE POSTERIOR BUT RESIDENCY THE DUBLY SO THE DOSTERIOR BUT AUTOPOD, IN THE AUTOPOD, DYNAMIC EXPRESSION OF THE DISTABLE BURSHORY OF THE DEVELOPMENT, EXPRESSION ENTRY OF THE DUBLY SO THE POSTERIOR BUT ANTER DUBLY SO THE POSTERIOR AND TO THE POSTE
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                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: HEART AND AORTA.
-!- TISSUE SPECIFICITY: HEART AND AORTA.
-!- DEVELOPMENTAL STAGE: HIGH EXTRABBRRYONIC EXPRESSION IS DETECTED AT 7.5 DPC. IN THE MATERNALLY DERIVED DECIDUUM. ALSO DETECTED ALONG THE YOLK SAC VESSELS DOTING THE PROCESS OF REMODELING AT 9.5-10.0 DPC. WITHIN THE EMBRYO, DETECTED AT 7.5 DPC IN THE LATERAL MESODERM. ON DAY 8.5 PC. MESODERM. IN THE LATERAL REGION OF THE EMBRYO, EXPRESSED IN THE LATERAL MESODERM. ON DAY 9.5 PC SEPARATION OF THE SOMATIC AND SPLANCHNIC MESODERM AT THE LEVEL OF SEPARATION OF THE DEVELOPING CARDIOVASCULAR REGION, MOST ADMINISTED THROUGHOUT THE DEVELOPING CARDIOVASCULAR REGION, MOST ADMINISTED THROUGHOUT THE DEVELOPING CARDIOVASCULAR REGION, MOST ADMINISTED THROUGHOUT THE PREST AND SECOND AORTIC
                     BUD. IS INVOLVED IN THE DEVELOPMENT OF BRANCHIAL ARCHES, WHICH GIVE RISE TO UNIQUE STRUCTURES IN THE HEAD AND NECK. BINDS DNA ON E-BOX CONSENSUS SEQUENCE 5'-CANNTG-3'.
SUBMINIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. FORMS HOMODIMERS AND HETERODIMERS WITH TCF3 GENE PRODUCTS E12 AND E47, HANDI AND HEYI, HEYZ AND HEYL (HAIRY-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTION FACTORS.
CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 183
ONWARD DUE TO FRAMESHIFTS.
UPSTREAM REGULATOR OF SONIC HEDGEHOG (SHH) INDUCTION IN THE LIMB
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Developmental protein; Anglogenesis; Transcription regulation;
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HELIX-LOOP-HELIX MOTIF.
LG -> TA (IN REF. 2).
A -> P (IN REF. 1).
A -> G (IN REF. 2).
A -> G (IN REF. 2).
W; 584F0AF5DF367115 CRC64;
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EMBL; U43715; AAA86274.1; ALT_FRAME.
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InterPro; IPR001092; HLH_dim.
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92
156
166
217 AA;
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CONFLICT
SEQUENCE
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"Point mutations in the transmembrane domain of DjlA, a
membrane-linked DnaJ-like protein, abolish its function in promoting
colaric acid production via the Rcs signal transduction pathway.";
Mol. Microbiol. 25:333-944(1997).

-!- FUNCTION: CHAPERONE THAT MAY PLAY A ROLE IN THE CORRECT ASSEMBLY,
ACTIVITY AND/OR MAINTENANCE OF A NUMBER OF MEMBRANE PROTEINS,
INCLUDING TWO-COMPONENT SIGNAL-TRANSDUCTION SYSTEMS. MIGHT CO-
OPERATE MITH DNAK TO ACTIVATE THE RCS TWO-COMPONENT SYSTEM.
-!- SUBCELLULAR LOCATION: Type III membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelley W.L., Georgopoulos C.; "Positive control of the two-component RusC/B signal transduction network by DilA: a member of the DnaJ family of molecular chaperones in Bscherichia coli."; Mol. Microbiol. 25:913-931(1997).
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEXAIN+XIZ / MGIGES;
MEDLINE=97426617; PubMed+9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riby M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
May B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Systematic sequencing of the Escherichia coli genome: analysis of
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clarke D.J., Jacq A., Holland I.B.; ^{\circ} A novel DnaJ-like protein in Escherichia coli inserts into the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
2.8%; Score 7; DB 1; Length 217; 100.0%; Pred. No. 19; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytoplasmic membrane with a type III topology."; Mol. Microbiol. 20:1273-1286(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND SEQUENCE OF 1-45 FROM N.A. MEDLINE=96405649; PubMed=8809778;
                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DJLA OR B0055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
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                                      7; Conservative
                                                                                                                                                                                                     STANDARD;
                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                           204 LKSTVSS 210
                                                                                                              189 LKSTVSS 195
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
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                                                                                                                                                                                                   DJLA_ECOLI
P31680;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-K12
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yura T.
                                                                                                                                                                                      DJLA_ECOLI
                                          Matches
                       Best
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There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L->R: LOSS OF ACTIVATION OF RCS.
M->R: ONLY PARTIAL ACTIVATION OF RCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
D-alanine aminotransferase (EC 2.6.1.21) (D-aspartate aminotransferase) (D-amino acid aminotransferase)
                                                                                                                                                                                                                                                                                                                                                                                                      .
O
                                                                                                                                                                                   PROSITE; PS00636; DNAJ_1; FALSE_NEG.
PROSITE; PS50076; DNAJ_2; 1.
Chaperone; Transmembrane; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                80A0FC28F6D470DF CRC64;
                                                                                                                                                                                                                                            POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                 PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  LOSS OF ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 AA.
                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 7; DB 1
100.0%; Pred. No. 23;
tive 0; Mismatches
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                          J-DOMAIN.
                                                                                  EMBL; D10483; -; NOT_ANNOTATED_CDS. EMBL; AE000116; AAC73166.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                30579 MW;
                                                                                                            HSSP; P25685; 1HDJ.
EcoGene: EG11570; djlA.
Interpro: IPR001623; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transaminase) (DAAT).
                                                                                                                                                                                                                                                                                                                                271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=ATCC 10716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AKQKAQE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AKQKAQE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAAA_BACLI
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DOMAIN
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Clausiliidae; Alopiinae; Albinaria.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence and gene organization of the mitochondrial genome of the land snail Abinaria coerulea."; Genetics 140:1353-1356(1995).

-: CATALTIC ACTIVITY: NACH + ubiquinone = NAD(+) + ubiquinol.

-: SUBCELLULAR LOCATION: Integral membranc protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pfam; PF00361; Oxidored_q1: 1.
Oxidoreductase; NAD: Ubiquinone; Mitochondrion: Transmembrane.
SEQUENCE 307 AA: 34865 WW; CF27C405278CB92D CRC64;
                                                                                    PROSTE; PE001961; Anihotran_4; 1.
PROSTE; PS00770; An_TRANSFER_CLASS_4; 1.
Transferaes, Anihotransferaes; Pyridoxal phosphate.
BINDING 144 114
PYRIDOXAL PHOSPHATE (POTENTIAL).
SEQUENCE 283 AA; 31396 MW; 2CA8FA604FEDE9D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                 2.8%; Score 7; DB 1; Length 283; 100.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%; Score 7; DB 1; Length 307; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          0; Indels
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15-JUI.-1999 (Rel. 38, Last annotation update)
NADH-ublquinone oxidoreductase chain 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                      0; Mismatches
                                                    InterPro; IPR001544; Aminotran_4. Pfam; PF01063; aminotran_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96120351; PubMed=7498775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Albinaria coerulea (Land Snail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
               EMBL; U26947; AAB50428.1; -. HSSP; P19938; 1DAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X83390; CAA58306.1; -.
                                                                                                                                                                                                   Query Match
Best Local Similarity 100.v
Fre 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_Tax1D=42349;
                                                                                                                                                                                                                                                                                                                180 SISLSLL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 SISLSLL 224
                                                                                                                                                                                                                                                                                           75 KOKAQEA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion
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CAR BRARES
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                                                                                                                                                                                                                                                                                                                                                                                                                         Rasmussen A.S., Janke A., Arnason U., \mbox{\footnote{thm}} The mitochondrial DNA molecule of the hagfish (Myxine glutinosa) and
                                                                                                                                                                                                                                                      MEDLINE-97398704; PubMed-9254918; Delarbre C., Barriel V., Tillier S., Janvier P., Gachelin G.; "The main features of the craniate mitochondrial DNA between the ND1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Myxininae; Myxine.
                                                                                                                                                                                                                                                                                                                 the COI genes were established in the common ancestor with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delarbre C., Rasmussen A.S., Arnason U., Gachelin G.; "Complete sequence of the mitochondrial DNA of Myxine glutinosa."; Submitted (JUN-2000) to the EMBL/GenBank/UDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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0
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PRINTS: PR01436; NADHDHGNASE2.
Oxidoreductase: NAD: Ubiquinone: Mitochondrion; Transmembrane.
CONFLICT 205 205 I -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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5. 29;
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S -> C (IN REF. 2).
; DD123DADD1CF61EA CRC64;
             021078; 063918;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubjquinone oxidoreductase chain 2 (EC 1.6.5.3).
MTND2 OR ND2 OR NAD2 OR NADH2.
 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 7; DB 1
100.0%; Pred. No. 29;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: Y19527; CAA70717.1; -.
EMBL: Y15187; CAA75486.1; -.
EMBL: A404447; CAC20650.1; -.
InterPro; 1PR003917; NADHub_oxdrdctse2.
InterPro; 1PR001750; Oxidored_q1.
                                                                                                                             Myxine glutinosa (Atlantic hagfish).
                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. Evol. 14:807-813(1997).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-98210228; Pubmed-9541532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Evol. 46:382-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 AA; 38788 MW;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrate phylogeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inner membrane
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datches 7; Conserv
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=7769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 ISNSLIL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 ISNSLIL 275
                                                                                                                                                 Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IADA_ECOLI
P39377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOASPARTYL (L'BETA-ASPARTYL) DIPEPTIDES. USED TO DEGRADE PROTEINS DAMAGED BY L-ISOASPARTYL RESIDUES FORMATION.
SUBCELLULAR LOCATION: CYLOplasmic.
SIMILARITY: SOME, IN THE N-TERMINAL, TO DIHYDROROTASE.
                                                                                                                                    STRIN-K12 / W3110;
MEDLINE=9518177; Pubmed-7876157;
Gary J.D., Clarke S.;
"Purification and characterization of an isoaspartyl dipeptidase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                 Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L., Blattner F.R., "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
-i. FUNCTION: CATALYZES THE HYDROLYTIC CLEAVAGE OF A SUBSET OF L-
                                                   Escherichia coli.
Bacteria; Protecbacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8%; Score 7; DB 1; Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 49.0 kDa protein F32B6.9 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Metalloprotease; Complete proteome.
SEQUENCE 390 AA; 41084 MW; 9CEEC838381545B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M38.
16-ocr-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae; Peloderinae; Caenorhabditis.
               Isoaspartyl dipeptidase (EC 3.4.19.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                Biol. Chem. 270:4076-4087(1995).
                                                                                                                                                                                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed-7610040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE000503; AAC77284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U15029; AAC43299.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U14003; AAA97224.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 ISKLLPT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 ISKLLPT 95
                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YV4Q_CAEEL
045435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20150255; Pubmed-10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Lihher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Relioflavin blosynthesis protein ribA (Includes: GTP cyclohydrolase II (EC 3.5.4.25); 3.4-dihydroxy-2-butanone 4-phosphate synthase (DHBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: GTP + 3 H(2)0 = formate + 2,5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine + diphosphate.
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.", Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
Basham V.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BESTROPHIN FAMILY.
                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 413 AA; 48965 MW; A66E69A83C78790B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 7; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                        WormPep; F3286.9; CE09864.
InterPro: JPR000615; Worm_fam_8.
Pen; PF01062; Worm_family_8; I.
ProDom; PD002802; Worm_fam_6; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
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SEQUENCE OF 550-588 FROM N.A.
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                                                            Escherichia coli, and
Escherichia coli 0157:H7
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                                                                                                                                           NCBI_TaxID=562, 83334;
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    between the Swiss Institute of Bioinformatics and the BMBL outstation.

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Brown A.E., Jackson P.J.;
                                                                                                                   Multifunctional enzyme; Řiboflavin biosynthesis; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.8%; Score 7; DB 1; Length 482; Best Local Similarity 100.0%; Pred. No. 39; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                            2.8%; Score 7; DB 1; Length 424
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SEQUENCE . 482 AA; 57210 MW; E473BDIFDCA73315 CRC64;
                                                                                                                                                                                GTP CYCLOHYDROLASE II.
0298128162BAC016 CRC64;
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Bacillus/Staphylococcus group; Bacillus.
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical trans-acting regulator pxo2-53.
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(Rel. 04, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 35;
Americal Conservative 0; Mismatches
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STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia Coli
Peptidoglycan synthetase ftsI precursor (Penicillin-binding protein 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura M., Maruyama I.N., Soma M., Kato J., Suzuki H., Horota Y.; "On the process of cellular division in Escherichia coli: nucleotide sequence of the gene for penicillin-binding protein 3."; Mol. Gen. Genet. 191:1-9(1983).
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STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
BIBLINE-FR., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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STRAIN-0157-H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; Pubbed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Pottamousis K.,

Apodaca J., Anartharana T.S., Lin J., Yen G., Schwartz D.C.,

"Concentry of the property of the proportion of the property of the p
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"FtsL, an essential cytoplasmic membrane protein involved in cell
                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                            FTSI OR PBPB OR B0084 OR 20094 OR ECS0088.
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J. Bacteriol. 174:7716-7728(1992).
[8]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90328986; PubMed-2198024; Michaud C., Parquet C., Flouret B., Blanot D., van Heijenoort J.; Mevised interpretation of the sequence containing the murp gene encoding the UDP-N-acetylmuramyl-tripeptide synthetase of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagasawa H., Sakagami Y., Suzuki A., Suzuki H., Hara H., Hirota Y.;
"Detecrmination of the cleavage site involved in C-terminal processing
of penicillin-binding protein 3 of Escherichia coli.";
J. Bacteriol. 171:5890-5893(1989).
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And mainto acid substitution in penicillin binding protein 3 creates
pointed polar caps in Escherichia coll.";
J. Bacteriol. 170:4828 4837 (1988).
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SIMILARITY: BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Membrane topology of penicillin-binding protein 3 of Escherichia
                                                                                                                                                                                                                                                                           Houba-Herin N., Hara H., Inouye M., Hirota Y.;
Binding of penicillin to thiol-penicillin-binding protein 3 of
Escherichia coli: identification of its active site.";
Mol. Gen. Genet. 201499-504 (1985).
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                                                                                                                                                                                                                                              MEDLINE-86117937; PubMed-3911028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90036670; PubMed=2681146;
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EMBL, X55034; CAA38861.1; -.
EMBL, D10483; BAA01349.1; -.
EMBL, AE000118; AAC73195.1; -.
EMBL, AE005185; AAC54388.1; -.
EMBL, AP002550; BAB33511.1; -.
                                                                                                                                                       Biochem. J. 269:277-280(1990).
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Pfam; PF00905; Transpeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S49802; AAB24312.1; -. EMBL; S49875; AAB24310.1; -. EMBL; X55814; CAA39333.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowler L.D., Spratt B.G.;
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S40594; S40594.
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                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94327513: PubMed-8051052;
Lee K.S., Patton J.L., Fido M., Hines L.K., Kohlwein S.P.,
Ladituf F., Henry S.A., Levin D.E.;
"The Saccharomyces cerevisiae PLB1 gene encodes a protein required for lysophospholipase and phospholipase B activity.";
J. Biol. Chem. 269:19725-19730(1994).
Inner membrane; Peptidoglycan synthesis; Cell division; Cell wall;
Antibiotic resistance; Multifunctional enzyme; Cell shape;
                                                                                                                                                           S->C: STILL ABLE TO BIND PENICILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Lysophospholipase 1 precursor (EC 3.1.1.5) (Phospholipase B 1).
PLB1 OR YMR008C OR YM8270.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)0 = glycerophosphocholine + a fatty acid anion. . -!- SUBCELLULAR LOCATION: Secreted. -!- SIMILARITY: TO OTHER FUNGAL LYSOPHOLIPASES AND TO YEAST
                                                                                                                                N -> S (IN MUTANT PBPBR1).
S->A,T: UNABLE TO BIND PENICILLIN.
                                         PEPTIDOGLYCAN SYNTHETASE FTSI.
                                                                                                                                                                                                                   Score 7; DB 1; Length 588;
Pred. No. 47;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                        C89A403D5980B2CD CRC64;
                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                    PERIPLASMIC (POTENTIAL).
                                                                                                                   ACYLATED BY PENICILLIN
                                                                                                                                                                                                                                                                                                                                                                               664 AA.
                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
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                           fransmembrane; Complete proteome.
                                                                                                                                                                                                                    2.8%;
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InterPro; IPR002642; PLAC.
Pfam; PF01735; PLA2_B; 1.
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588 AA;
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                                                                                                                                                                                                                                                                                                        354 GVLQKSS 360
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                                                                                                                                                                                                                                                                            63 GVLQKSS 69
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P39105;
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TRANSMEM
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VARIANT
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Eukaryota, Fungi, Ascomycota; Saccharomycotes;
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(POTENTIAL).
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01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 80.2 kDa protein in CPA2-NNF1 intergenic region.
YJR110W OR J2007.
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rose M., Koetter P., Entian K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                E05A585E7AB73F34 CRC64;
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            Glycoprotein; Signal. POTENTIAL.
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100.0%; Pred. No. 53;
ative 0; Mismatches
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InterPro; IPR000340; DS_phosphatase.
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              Lipid degradation; Hydrolase;
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SMART; SM00022; PLAC; 1
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123
160
170
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ses 7: Conserv
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CONFLICT
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Chen S., West R.W. Jr., Johnson S.L., Gans H., Kruger B., Ma J.;
TSTS, a global regulatory protein that silences transcription of
yeast GAL genes, also mediates repression by alpha 2 repressor and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harashima S., Mabuchi H., Ramash R., Hasebe M., Tanaka A., Oshima Y.; Suhmitted (AUG-1992) to the {\rm EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                              Gaps
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"The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading frames including a novel gene encoding a globin-like domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 12:1071-1076(1996).
-!- FUNCTION: GLOBAL REGULATORY PROTEIN THAT SILENCES TRANSCRIPTION
OF GAL AND MATING-TYPE GENES. NEGATIVE REGULATOR OF THE HO
(HOWOTHALLISM) GENE. MAY POTENTIATE TRANSCRIPTIONAL ACTIVATION
AND REPRESSION BY REGULATING THE ACTIVITY OF THE BASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93024394; PubMed-1406639; Jiang Y.W., Stillman D.J.; Jiang Y.W., Stillman D.J.; Involvement of the SIN4 global transcriptional regulator in the chromatin structure of Saccharomyees cerevisiae."; Mol. Cell. Biol. 12:4503-4514(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Global transcriptional regulator SIN4.
SIN4 OR TSF3 OR BEL2 OR GAL22 OR SSF5 OR YNL236W OR N1135.
                                                                                                                                                       DB 1; Length 688;
                                                                                                                                                                                            0; Indels
                                                                                                A097F4B98B626C01 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       974 AA
                                                                                                                                                   2.8%; Score 7; DB 1
100.0%; Pred. No. 54;
tive 0; Mismatches
                                                                             BY SIMILARITY
                  SMART; SM00012; PTPC_DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
Hypothetical protein; Hydrolass
ACT_SITE
SEQUENCE 688 AA; 8015; MW; A097F4B9!
InterPro; IPR000387; TYR_phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 13:831-840(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHÖUENCE FROM N.A.
MEDLINE-97051596; Pubmed-8896273;
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Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yeast GAL genes, als
identical to SIN4.";
Mol. Cell. Biol. 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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RESULT 26
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                                                                                                                                                                                                                               NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). ; 12ECF5E4CDC05A8E CRC64;
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the left arm of chromosome XIV from Saccharomyces cerevisiae.";
Yeast 13:849-860(1997).
-!- FUNCTION: INTERACTS WITH THE SNF1 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94173726; PubMed=8127709; Lesage P., Yang X., Carlson M.; Landlysis of the SIP3 protein identified in a two-hybrid screen for interaction with the SNRI protein kinase."; Nucleic Acids Res. 22:597-603(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the 33 kb long region between ORC5 and SUII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                SGD: S0005180; SIN4.
Transcription regulation; Activator; DNA-binding; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S2288C / FY1679;
MEDLINE-97377992; PubMed-9234673;
Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler T.A.,
Hegemann J.H.;
                                                                                                                                                                                                                                                                                          2.8%; Score 7; DB 1; Length 974; 100.0%; Pred No. 75;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                   SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: STRONG, TO YEAST YHRISSW.-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                            974 AA; 111296 MW;
           EMBL; M93050; AAA35044.1; -... EMBL; X64716; CAA45819.1; EMBL; D12918; BAA02302.1; -... EMBL; Z69381; CAA93362.1; -... EMBL; Z71512; CAA940.1; -...
                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03376; AAA17885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X96722; CAA65487.1; -. EMBL; Z71533; CAA96164.1; -.
                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIP3 protein.
SIP3 OR YNL257C OR N0844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                               893
                                                                                       PIR; A44484; A44484.
PIR; S20132; S20132.
                                                                                                                    A48074; A48074.
S41805; S41805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                   TRANSFAC; T01243;
                                                                                                                                                                                                                                                                                                                                                                                    859 GLKISNS 865
                                                                                                                                                                                                                                                                                                                                                     101 GLKISNS 107
                                                                                                                                                                                                 Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIP3_YEAST
P38717;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                            Ouery Match
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                DOMAIN
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                                                                                                                      PIR;
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Rey I., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte E.,
Guilbaud R., Jacquet M., Tocque B.;
"The CoOH-domain of the product of the Saccharomyces cerevisiae SCD25
gene elicits activation of p21-ras proteins in mammalian cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crechet J.B., Poullet P., Mistou M.-Y., Parmeggiani A., Camonis J., Boy-Marcotte E., Damak F., Jacquet M.; Enhancement of the GDP-GTP exchange of RAS proteins by the carboxylterminal domain of SCD25."; Science 248:866-868(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANBOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 RASGEP DOMAIN.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Damak F., Boy Marcotte E., le Roscouet D., Guilbaud R., Jacquet M.; "SDC25, a CDC25-1ike gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae."; Mol. Cell. Biol. 11:202-212(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.; "The C-terminal part of a gene partially homologous to CDC 25 gene suppresses the cdc25-5 mutation in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 6:347-349(1991).
-! FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
                                                                                                                                                                                                       Length 1229;
                                                                                                                                                                                                                                         0; Indels
                                                                                                                                            142819 MW; 977995219282CD65 CRC64;
                                                                                                                                                                                                   DB 1;
lo. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                   2.8%; Score 7;
PIR; S42391; S42391.
SGD; S0005201; SIP3.
InterPro; IPR001849; PH.
Pfam; PF00169; PH; 1.
SWART; SM00233; PH; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91094833; PubMed=1986220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89306677; PubMed=2545538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 668-1253 FROM N.A.
                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCD25 OR SDC25 OR YLL016W
                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                          SEQUENCE 1229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sene 77:21-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          146 LKASLDL 152
                                                                                                                                                                                                                                                                                                          190 LKASLDL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID*4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCD25 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0L136;
                                                                                                                                                                                                                                                                                                                                                                                                       SC25_YEAST
P14771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-W303
                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                 Guanine-nucleotide releasing factor; Cell cycle; Cell division;
                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                  434 437 POLY-ARG,
584 590 DVVVKFI -> V (IN STRAIN 05.136).
1253 AA: 144979 MW; 2DE2C9EC27E3E60D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obermaier B., Gassenhuber J., Piravandi E., Domdey H.; Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevisiae chromosome II."; reast 11:1103-1112(1995).
                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 7; DB 1; Length 1253; 100.0%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contreras R., Fiers W., Logghe M., Molemans F.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION, AND SEQUENCE OF 117-133 AND 153-166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales: Saccharomycetaceae; Saccharomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleoporin NUP170 (Nuclear pore protein NUP170).
NUP170 OR YBL079W OR YBL0725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1502 AA.
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                             SH3.
POLY-ASN.
POLY-ARG.
                                                                                      SGD; S0003939; SDC25.
InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96076635; PubMed-7502586;
                                                                                                                                                                                                                     PROSITE; PS00720; GDS_CDC25; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1262-1502 FROM N.A.
                                                               EMBL; M26647; AAA16565.1; -. PIR; S14177; S14177.
                                                                                                                                                                               SMART; SM00147; RasgeF; 1.
SMART; SM00229; RasgeFn; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                          Pfam; PF00617; RasGEF; 1.
Pfam; PF00618; RasGEFN; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                 InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                             98
79
437
590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        149 SLDLLTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C;
                                                                                                                                                                                                                                                                  SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N170_YEAST
ID N170_YEAST
AC P38181;
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The single transmembrane segment of gp210 is sufficient for sorting to the pore membrane domain of the nuclear envelope.";
J. Cell Biol. 119:1441-1449(1992).
-:- SUBCELLULAR LOCATION: MEMBRANE-BOUND. NUCLEAR PORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primary structure analysis of an integral membrane glycoprotein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTEGRAL MEMBRANE GLYCOPROTEIN GP210.
CISTERNAL SIDE (PROBABLE).
-!- SIMILARITY: TO YEAST NUP157, AND SOME, TO MAMMALIAN NUP155.
                                                                                                                                                                                                                                                                                                                                                                     ·,
                                                                                                                                                                                                                                                                                                                                Length 1502;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                      Nuclear protein; Transport.
SEQUENCE 1502 AA; 169474 MW; 3BEA65DAA2A5F99A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Transmembrane; Nuclear protein; Signal.
                                                                                                                                                                                                                                                                                                                           Query Match
2.8%; Score 7; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2001 (Rel. 40, Last annotation update)
Integral membrane glycoprotein gp210 precursor.
                                                                                                                                              or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89291948; Pubmed=2738089;
Wozniak R.W., Bartnik E., Blobel G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the nuclear pore.";
J. Cell Biol. 108:2083-2092(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93107146; PubMed-1281815;
                                                                                                                                                                              EMBL; X79489; CAA56029.1; -.
                                                                                                                                                                                                    Z35840; CAA84900.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y00826; CAA68759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003343; Big_2.
Pfam; PF02368; Big_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wozniak R.W., Blobel G.;
                                                                                                                                                                                                                     PIR; S45429; S45429.
SGD; S0000175; NUP170.
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1886
1805
1828
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                                                                                                                                                                                                                                                                                                                                                                                                  206 STVSSLL 212
                                                                                                                                                                                                                                                                                                                                                                                                                           723 STVSSLL 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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26
1806
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P11654;
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RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broxstein P., Botshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broxstein P., Shottier P.,
RA Borkova D., Botchar W., Denma D.A., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence similarity of the amino-terminal domain of Drosophila beta spectrin to alpha actinin and dystrophin."; J. Cell Biol. 109:1633-1641(1989).
                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                   (POTENTIAL).
                                                   (POTENTIAL)
                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                            Length 1886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Byers T.J., Husain-Chishti A., Dubreuil R.R., Branton D., Goldstein L.S.B.;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                       6920B93C20A6C5D1 CRC64;
                                                               N-LINKED GLCNAC...)
   CYTOPLASMIC (PROBABLE)
                                                                                                                                                                                                                                                                     Query Match
2.8%; Score 7; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                        (GECNAC.
                N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                    N-LINKED (
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MEDLINE=90009037; PubMed=2677025;
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NCBI_TaxID=7227;
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hermadez J.R., Houck J., Howland T.J., Hermadez J.R., Houck J., Howland T.J., Hermadez J.R., Houck J., Howland T.J., Hermadez J.R., Houch D., Laiz J., Lidla M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Laiz Z., Kalp D., Laiz Z., Kalp D., Laiz J., Lidla Y., Mosherson D., R.A. Metson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Reinert K., Remington K.S., Panla Y., Pollard J., Puril Y., Reese M.G., Rahe B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T., Spher E., Spradling A.C., Staplecon M., Strong R., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Malliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.F., Zaveri J. S., Zhan M., Zhang G., Zhang L., Rang Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Rang Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., R. The genome sequence Of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE-8805942; PubMed-3680372;
MEDLINE-8805942; PubMed-3680372;
Dubreuil R., Byers T.J., Branton D., Goldstein L.S.B., Kiehart D.P.;
"Drosophilia spectrin. I. Characterization of the purified protein.";
J. Cell Biol. 105:2095-2102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96164435; PubMed-8591029;
Zhang P., Talluri S., Deng H., Branton D., Wagner G.;
"Solution structure of the pleckstrin homology domain of Drosophila
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InterPro, IPR001589; Actinin_act_bind.
InterPro; IPR001715; Calponin_hom.
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InterPro; IPR002017; Spectrin.
InterPro; IPR001605; Spectrin_PH.
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EMBL, ARD03306; AF48751.1; -.
PIR, A33657; A33657
PIR, A46147.
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Pfam; PF00169; PH; 1.
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MEDIINE-91302479, PubMed-1906475, Nishiyama A., Dahlin K.J., Prince J.T., Johnstone S.R., Stalloup W.B., "The primary structure of NG2, a novel membrane-spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 2047-2096.
Nishiyama A., Dahlin K.J., Prince J.T., Johnstone S.R., Stallcup W.B.;
J. Cell Biol. 145:1115-1115(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rai).
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Chondroitin sulfate profeoglycan NG2 precursor (HSN tumour-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 30-47; 1011-1016 AND 1466-1477.
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                                                      PROSITE; PS50021; CH; 2. PROSITE; PS50003; PH_DOMAIN; 1. Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
                                                                                                    ACTIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 7; DB 1; Length 2291; 00.0%; Pred. No. 1.6e+02; ve 0; Mismatches 0; Indels
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265737 MW; 5CDFB0C548BBC39B CRC64;
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SPECTRIN 2.
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SPECTRIN 6.
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SPECTRIN 7.
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SPECTRIN 9.
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SPECTRIN 11.
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SPECTRIN 15.
SPECTRIN 16.
SPECTRIN 17.
                                                                                        Capping protein; Repeat; 3D-structure. DOMAIN 1 271
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                                PROSITE; PS00019; ACTININ_1; 1. PROSITE; PS00020; ACTININ_2; 1.
                       SM00150; SPEC; 16.
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 SMART; SM00033; CH; 2.
SMART; SM00233; PH; 1.
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"The chondroitin sulfate proteoglycan NG2 is a tumour-specific antigen on the chemically induced rat chondrosarcoma HSN.";

Int. J. Cancer 58:700-705(1994)

Int. J. Cancer 68:700-705(1994)

Int. ACARE CHONDROITIN SULFATE PROTEOGLYCAN OF 400-800 KDA WITH A CORE PROTEIN SIZE OF 300 KDA.

INT. SUBCELLULAR LOCATION: Type I membrane protein.

INT. SUBCELLULAR LOCATION: Type I membrane protein.

INT. DEVELOPMENTAL STAGE: THE LEVEL OF EXPRESSION IS HIGHEST ON IMMATURE, PROLIFERATING CELLS AND DECREASES AS THESE CELLS DIFFERENTIATE.
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(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
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POTENTIAL.
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LAMININ G-LIKE 1.
LAMININ G-LIKE 2.
ASP/GLU-RICH (ACIDIC).
GLY/SER-RICH (GLYCOSAMINOGLYCAN
ATTACHMENT DOMAIN) (POTENTIAL).
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Glycoprotein; Transmembrane; Proteoglycan; Signal; Repeat.
SIGNAL
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100.0%; Pred. No. 1.6e+02;
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4 X REPEATS, A-TYPE.
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Best Local Similarity 100.0%; Pred. NO. ...
Matches 7; Conservative 0; Mismatches
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InterProc; IPR0001791; Laminin.G.
Pfam; PP00054; laminin.G; 1.
SMART; SM00282; LamG; 2.
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RESULT 33
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                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit (BC 2.1.1.86) (NS-methyltetrahydromethanopterin B-methyltransferase 28 kDa subunit methyltransferase 28 kDa subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea, Saturniidae, Saturniinae, Antheraea.
                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS ENYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ou X.-M., Steiner H., Engstroem A., Bennich H., Boman H.G.;
Insect immunity: isolation and structure of cecropins B and D from
pupe of the Chinese cak silk moth, Antheraea pernyi.";
Eur. J. Biochem. 127:219-224(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                             MEDLINE=96370840; PubMed=8774736; Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.; "Sodium ion translocation by N5-methyltetrahydromethanoperin: ocenzyme M methyltransferase from Methanosarcina mazei Gol reconstituted in ether lipid liposomes."; Eur. J. Biochem. 239:857-864(1996).
                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Methyltransferase; Transmembrane; Methanogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 6; DB 1; Length 12; 100.0%; Pred. No. 14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 (methylthio)ethanesulfonate.
-1- SUBGNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA; 1321 MW; 6DE4A5766232D76B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                     Methanosarcina mazei (Methanosarcina frisia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antheraea pernyi (Chinese oak silk moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=83053368; PubMed=6754375;
                                                                                                                                                                                                                                                                                                                                                                                                TETRAHYDROMETHANOPTERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity lub.v.
6; Conservative
                                                                                     STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                   STRAIN=DSM 3647 / GOE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE.
                                                                                                                                                                                                                                NCBI_TaxID=2209;
124 NLSFPVT 130
                     773 NLSFPVT 779
                                                                                                                                                                                                                   Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 KLEPVL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KLEPVL 8
                                                                                     TM2A METMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cecropin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CECB_ANTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                        SECUENCE
                                                                                              P80652:
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MEDLINE-88108273; PubMed-2962676;

Craig A.G., Engstrom A., Bennich H., Kamensky I.;

Plasma desorption mass spectrometry coupled with conventional peptide sequencing techniques.";

Biomed Environ. Mass Spectrom. 14:669-673(1987);

-i- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST SEVERAL GRAM-POSITIVE AND CRAM-NEGATIVE BACTERIA.

-i- SMILLARITY: BELONGS TO THE CECROPIN FAMILY.

PIR: A01771; CKAOBP.

PIR: A54725; A54725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nentwig W.;
"CSTX.9, a toxic peptide from the spider Cupiennius salei: amino acid sequence, disulphide bridge pattern and comparison with other spider toxics containing the cystine knot structure.";
cell. Mol. Life Sci. 58:1538-1545(2001).
'- FUNCTION: THIS TOXIN CAUSES PARALYSIS IN DROSOPHILA WITH AN LD50 VALUE OF 3.12 PMOL/MG.
'- SUBCELLULAR LOCATION: Secreted.
'- TISSUE SPECIFICITY: Produced by the venomous gland.
'- TISSUE SPECIFICITY: Max.5529.75; MW_ERR=0.32; METHOD=Electrospray.
                                                                                                                                                                                                                                                                                                                                                         Probom; PD003996, ITP_ceropin; 1.
PROSITE; PS00268; CECROPIN: 1.
Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
35 35 AMIDATION.
SEQUENCE 35 AA; 3818 MM; 7AFCBB0A10E16313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21544892; PubMed-11693532;
Schaller J., Kaempfer U., Schuerch S., Kuhn-Nentwig L., Haeberli S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, DISULFIDE BONDS, MASS SPECTROMETRY, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuplennius salei (Wandering spider).
Eukaryota: Metazoa: Arthropoda; Chelicerata: Arachnida: Araneae;
Araneomorphae: Entelegynae: Lycosoidea; Ctenidae; Cupiennius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 35; ). 38;
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100.0%; Pred. No. 69;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 46
68 AA; 7539 MW; 5BB526DCA359F9F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%; Score 6; DB 1
100.0%; Pred. No. 38;
tive 0; Mismatches
                                                                                                                                                                                                                                                                          InterPro; IPR000875; Cecropin.
InterPro; IPR03254; IIP_cecropin.
Pfam; PF00272; Cecropin; 1.
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Matches 6: Conservative
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48
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Best Local Similarity
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DISULFID 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID = 6928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 VAVLGE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 SSLLQK 214
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                                                                                                                                                                                                                                                                 Berger D.K., Woods D.R., Kawlings D.E.;
"Complementation of Escherichia coli sigma 54 (NtrA)-dependent
formate hydrogenlyase activity by a cloned Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- FUNCTION: INVOLVED IN NUCLEAR, BASIC PROTEIN TRANSITION: HISTONES ARE REPLACED BY SPERMATID SPECIFIC PROTEINS WHICH ÁRE THEMSELVES REPLACED BY PROTAMINES IN LATE SPERMATIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last acquence update)
01-FBB-1991 (Rel. 17, Last annotation update)
01-FBB-1991 (Rel. 17, Last annotation update)
Spermatid-specific protein S2 (Basic nuclear protein S2).
Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
Elasmobranchii: Galeomorphii: Galeomorphii: Galeomorphii: Galeomorphii: Galeomorphiis Galeomorphiis Galeomorphiis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chauviere M., Martinage A., Briand G., Sautiere P., Chevaillier P., "Nuclear basic protein transition during sperm differentiation. Primary structure of the spermatid-specific protein S2 from the
                                                                                                                                                                                                                                                                                                                                                                          -! SIMILARITY: BELONGS TO THE SIGMA(54) MODULATION PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 172:4399-4406(1990).
                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                     01-MAR-1992 (Rel. 21, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Probable sigma(54) modulation protein (ORF3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 78; . 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 78 AA, 8751 MW; F39C7C4944E413EB CRC64;
                                    78 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4%; Score 6;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003489; Ribosomal_S30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dog-fish Scylliorhinus caniculus.";
Eur. J. Biochem. 180:329-335(1989).
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKT;
                                                                                                                                                                                                                                 STRAIN=ATCC 33020;
MEDLINE=90330545; PubMed+2198257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89170733; PubMed-2924768;
                                                                      01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF02482; Ribosomal_S30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMFL; M58480; AAA27380.1; -.
                                                                                                                                            Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C37761; C37761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                            NCBI_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 LSNVVD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 LSNVVD 54
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9
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                                    RP5M_THIFE
P24694;
                                                                                                                                                                                                                                                                                                                          ntrA gene.
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RESULT 34
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14 pothetical 9.2 kDa protein in cysT-cysR intergenic region (ORF 81).
Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
-!- MISCELLANEOUS: N-TERMINAL HALF IS HIGHLY BASIC, WHILE C-TERMINAL
                              -i- SIMILARITY: WITH PROTEIN SI (70% STRUCTURAL SIMILARITY).
PIR; S03560; S03560.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization and mutagenesis of sulfur-regulated genes in a
                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyanobacterium: evidence for function in sulfate transport.";
J. Bacteriol. 173:2739-2750(1991).
-i. FUNCTION: MAY HAVE A REGULATORY FUNCTION.
-i. SIMILARITY: TO SYNECHOCYSTIS PCC 6003 SSR2439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                           DB 1; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfate transport, Hypothetical protein.
SEQUENCE 81 AA; 9251 MW; 2F3EEC6E3E82C146 CRC64;
                                                                                                     80 AA; 9733 MW; 593E18EF33452409 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
80S ribosomal protein S20.
RPST OR MPN541 OR MP301.
                                                                                                                                                                            90;
                                                                                                                                                        2.4%; Score 6; DB 1
100.0%; Pred. No. 80;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91210162; Pubmed=1708375;
Laudenbach D.E., Grossman A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M65247; AAA73045.1; -.
                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D43670; D43670.
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                PART IS ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1140;
                                                                                    Nuclear protein.
                                                                                                                                                                                                                               47 VDNT1.K 52
                                                                                                                                                                                                                                                               55 VDNTLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LTGTSE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 LTGISE 57
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                                                                                                                                                                                                                                                                                                                                                   YO39_SYNP7
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                    Y039_SYNP7
                                                                                                                                                                                           Matches
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S % ₹ ₹ 9000
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MIM; 605354; -.
                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ICEBERG: a novel inhibitor of interleukin-lbeta generation.";
Cell 103:99-111(2000).
-!- FUNCTION: INHIBITS GENERATION OF IL-1BETA BY INTERACTING WITH
CASPASE-1 AND PREVENTING ITS ASSOCIATION WITH RIP2.
-!- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN THE HEART AND PLACENTA.
-!- SIMILARITY: CONTAINS I CARD DOMAIN.
                                                                                                                                                                                 "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                        Nucleic Acids Res. 24:4420-4449(1996).
-!- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity).
-!- SIMILARITY: BELONGS TO THE S20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humke E.W., Shriver S.K., Starovasnik M.A., Fairbrother W.J.,
                                                                                                                                    Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 87; . 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan: PF01649; Ribosomal_S20p; 1.
Profom: PD004231; Ribosomal_S20p; 1.
Ribosomal protein: rRNA-binding: Complete proteome.
SEQUENCE 87 AA; 9970 WW; 4CAB26530C6B1D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 6; DB 1
100.0%; Pred. No. 87;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000028; AAB95949.1; -. InterPro; IPR002583; Ribosomal_S20p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=20503847; Pubmed=11051551;
                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF208005; AAG23528.1; -.
Mycoplasmataceae, Mycoplasma
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caspase-1 inhibitor Iceberg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LDNLGN 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 LDNLGN 46
                                                                                                                                                                                                            pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICBR_HUMAN
P57730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 38
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller N., Waterston R.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 10.2 kDa protein C28H8.8 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 91; 0. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                     DB 1; Length 90;
                                                                                                                                                  7E74C74263367101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10199 MW; BD4D391C6D1B1DAD CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                        2.4%; Score 6;
100.0%; Pred. No
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                                                                                                                              CARD.
                                                                                                                                                SEQUENCE 90 AA; 10138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U20861; AAA62296.1; -.
WormPep; C28H8.8; CE01830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein AF0249. AF0249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR002485; DUF13.
Pfam; PF01482; DUF13; 1.
ProDown; PD002726; DUF13; 1.
InterPro: IPR001315; CARD. Pfam; PF00619; CARD; 1. SMART; SMO0114; CARD; 1.
                                                                          PROSITE; PS50209; CARD; 1.
                                                                                                Thiol protease inhibitor.
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 91 AA; 10
                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                               221 RIFIHS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 LDVKAE 115
                                                                                                                                                                                                                                                                                                                                                              11 RIFIHS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 LDVKAE 38
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16-0CT-2001
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029990;
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                                                                                                                                          Richard H. P. Clayton R.A. Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Relaschmann R.D., Quackenbab J., Lee N.H., Sutton G.G., Gill S., Rirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., Moneil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea R.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                  Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.4%; Score 6; DB 1; Length 92; 100.0%; Pred. No. 91; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
SEQUENCE 92 AA; 10460 MW; 71BC209B54679EDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYLE protein (Dexamethasone-induced protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 AA.
                                                                                                           STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001088; AAB90984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Renal cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                             SEQUENCE FROM N.A.
                                                      NCBI_TaxID=2234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 EKLKVD 13
                                  Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
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                                                                                                                                                                                                                                                                                                                                           Venter J.C
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Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Radota K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Hrownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
M. Washina Y., Washida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Medazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                         2.4%; Scure 5; DB 1; Length 95;
100.0%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                          EMBL; AF108145; AAC83382.2; -.
EMBL; BC001083; AAH01083.1; AL7_INIT.
SEQUENCE 95 AA; 10429 MW; F9F98DE2572U3F83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYLE protein (Dexamethasone-induced protein). MYLE OR DEXI.
                                                                                                                                                                                                   100.0%; Pred. ....
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EMBL; AK007644; BAB25159.1; ALT_INIT.
MGD; MGI:1926236; Myle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Pancreas;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                               60 VDLGVL 65
                                                                                                                                                                                                                                                                                                       68 VDLGVI, 73
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                                                                                                                                                                                                                                                                                                                                                                                                MYLE_MOUSE
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Davis R.W.;
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                                                                                                                                                                                                                        Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                    Gaps
                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato)
Skaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                             Pear J.R., Ridge N.P., Rasmussen R., Rose R.E., Houck C.M.; "Isolation and characterization of a fruit-specific cDNA and the corresponding genomic clone from tomato."; plant Mol. Biol. 13:639-651(1989).
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0
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                             2.4%; Score 6; DB 1; Length 95; 100.0%; Pred. No. 94; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.4%; Score 6; DB 1; Length 96;
95 AA; 10402 MW; 4F293AD7F2326B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10699 MW; F6B2BF5D0A955FA6 CRC64;
                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Fruit-specific protein.
                                                                                                                                                96 AA.
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16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 95; tive 0; Mismatches
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. UC82B: TISSUE-Fruit;
MEDLINE-91370848; PubMed-2491680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13743; CAA32007.1; -.
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                                                    6; Conservative
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                                                                                                                                                STANDARD;
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                             Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                              NCBI_TaxID=4081;
                                                                        60 VDLGVL 65
                                                                                            68 VDLGVL 73
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SEQUENCE 96
                                                                                                                                                FSPM_LYCES
P14903;
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Q46404;
 SEQUENCE
                                                                                                                           43
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MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalnan S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                         MEDLINE-95362647; PubMed-7543468;
Frahr M.J., Douglas A.L., Xia W., Hatch T.P.;
"Characterization of late gene promoters of Chlamydia trachomatis.";
J. Bacteriol. 177:4252-4260(1995).
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STATAN-KIZ / MG1655,
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 96;
0; Mismatches 0; Indels
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                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
16-OCT-2001 (Rel. 40, Last annotation update)
Late transcription unit B protein.
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101-NoV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yafN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.4%, Webst Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001282; AAC67671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L40838; AAA75630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Ohmori H.;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 SLLDKH 189
                                                                                                                                                                   NCBI_TaxID=813;
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                                                                                                                                                                                                                                                                     STRAIN-LGV434;
                                                                  LTUB or CT080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanbongi Y., Igarashi Y., Kodama T.; "Thermostablity of cytochrome c-552 from the thermophilic hydrogen-oxidizing bacterium Hydrogenobacter thermophilus."; Biochemistry 28:9574-9578(1989).
                                                                  Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydrogen-oxidizing bacterium, Hydrogenobacter thermophilis."; J. Bacteriol. 171:65-69(1989).
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                    Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
234 MW; C49811AE1E90A659 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrogenobacter thermophilus.
Bacteria; Aquificales; Aquificaceae; Hydrogenobacter.
NCBI_TaxID=940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanbongi Y., Ishii M., Igarashi Y., Kodama T.; "Amino acid sequence of cytochrome c-552 from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-AUC-1992 (Rel. 23, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
Cytochrome c-552 precursor (C552).
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MEDLINE=89123087; PubMed=2536668;
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                                                                                                                                                                                                                                                                                                                           EMBL; AE000131; AAC73336.1; -.
EMBL; U70214; AAB08652.1; -.
ECOGENE; EG1315; yafn.
Hypothetical protein; Complete
SEQUENCE 97 AA; 11234 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Best Local Similarity
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P15452;
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Hasegawa J., Yoshida T., Yamazaki T., Sambongi Y., Yu Y., Igarashi Y., Kodama T., Yamazaki W., Kyogoku Y., Kobayashi Y., Yamazaki W., Kyogoku Y., Kobayashi Y., Solution structure of thermostable cytochrome c-552 from Hydrogenobacter thermophilus determined by IH-NMR spectroscopy."; Blochmistry 77:964-1964[1988].

-i. FUNCTION: REACTS WITH HYDROGENASE.

-i. PUNCTION: REACTS WITH HYDROGENASE.
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MEDLINE-97283757; PubMed-9137835;
Wang S.L., Liu X.-Q., Douglas S.E.;
The large ribosomal protein gene cluster of a cryptomonad plastid:
gene organization, sequence and evolutionary implications.";
Biochem. Mol. Biol. Int. 41:1035-1044(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Douglas S.E., Penny S.L.; "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
F49713D829DDE927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Cryptophyta, Cryptomonadaceae, Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heme; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOCHROME C-552.
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-DEC-1998 (Rel. 37, Last sequence update)
-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COVALENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AA
                                                                                                                        -!- SIMILARITY: 56% WITH P.AERUGINOSA C551.
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InterPro: IPR000345; CytC_heme_bind.
InterPro: IPR001308; Cyt_Cl.
InterPro: IPR00224; Cyt_ClD.
Pfam; PF00034; Cyt_Chrome_c; I.
PRINTS; PR0066; CYTCHROMECID.
PRINTS; PR0066; CYTCHROMECID.
Electron transport; Heme; Signal; 3D-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast 50S ribosomal protein 124
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                                                                                                                                                                                                                                                                                            EMBL; X57735; CAA40902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 AA; 10431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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PIR; S32485; S32485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast.
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046905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
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DNA replication; Nuclear protein.
SEQUENCE 104 AA; 11793 MW; 377BCF913652F1AE CRC64;
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFA3_SCHPO STANDARD; PRT; 104 AA.
092374;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Replication factor-A protein 3 (Single-stranded DNA-binding protein

    Mol. Evol. 48:236-244(1999).
    SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.

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Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: BINDS TO SINGLE-STRANDED SEQUENCES.
-- SUBMIT: HETEROTRIMER OF 68, 30, AND 12 kDa CHAINS.
-- SUBCELLURAR LOCATION: NUClear.
                                                                                                                                                                                                                              Pfam: PF00467; Ribosomal_L24: 1.
Probom: PD001677; Ribosomal_L24: 1.
PROSITE: PS01109; RIBOSOMAL_L24; FALSE_NEG.
PROSITE: PS01109; RIBOSOMAL_L24; FALSE_NEG.
SEQUENCE 1 protein: Chloroplast.
SEQUENCE 101 AA: 11572 MW; 306E2E229C636131 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                   2.4%; Score 6; DB 1
100.0%; Pred. No. 99;
tive 0; Mismatches
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                                                                                                                                                                              EMBL; AF041468; AAC35714.1; ·.
InterPro; IPR003256; Ribosomal_L24.
InterPro; IPR000302; Ribosomal_L24_NusG.
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EMBL: AL109608: CAB51564.1: -
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Best Local Similarity
Thes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSB3 OR SPCC23B6.05C.
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                                                                                                                                                                                                                                                                                                                                                                                                                   105 SNSLIL 110
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. strain PCC6803. II. Sequence determination of the chiltre genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
-i. SIMILARITY: BELONGS TO THE YCF20 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region precursor.

Heterodontus francisci (Horn shark).

Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Chondrichthyes;

Elasmobranchii; Galeooncphii; Heterodontoidea; Heterodontiformes;

Heterodontidae; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Sequence analysis of the genome of the unicellular cyanobacterium
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             Db .,
le+02;
~~< 0; Indels
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     DB 1; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein; Complete proteome.
109 AA; 12555 MW; F353C5EDC854EE63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                              Y20L_SYNY3 STANDARD; PRT; 109 AA.
P72983;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (kcl. 37, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
2.4%; Score 6; DB 1
100.0%; Pred. No. 1e+
tive 0; Mismatches
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                                                         Conservative
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                      Local Similarity
nes 6; Conserva
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Best Local Similarity
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                                                                                                        46 TVDNTL 51
                                                                                                                                                          48 TVDNTL 53
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P03983;
     Query Match
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HV01_HETFR
                                                    Matches
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                                                                                                                  phylogenetically primitive shark.";
Proc. Natl. Acad. Sci. U.S.A. 82:2082-2086(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                            Lithman G.W., Berger L., Murphy K., Litman R., Hinds K.,
Erickson B.W.;
"Immunoglobulin VH gene structure and diversity in Heterodontus, a
                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK - 2.
COMPLEMENTARITY - DETERMINING - 2.
FRAMEWORK - 3.
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                                 SEQUENCE FROM N.A. (CLONE HXIA).
MEDLINE-85166276; PubMed-3920659;
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InterPro; IPR003596; Ig_v.
Pfam: PF00047; ig; l, Ig_r.
SMART; SM00406; IGv; l, Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                 EMBL; M12195; AAA49326.1; -.
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Best Local Similarity 100.0
Matches 6; Conservative
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NCBI_TaxID=7792;
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Search completed: August 6, 2002, 16:49:56 Job time: 223 sec

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095wy6 ixodes scap
096d14 mus musculu
096ff6 homo sapien
05253 amycolatops
06471 rattus norv
094fx0 glycine max
094fx1 glycine max
0977a9 metarhizium
09770 clostridium
09770 clostridium
097703 chlamydia p
091ry0 chlamydia p
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Q9c2q5 neurospora
Q92x04 rhizobium m
Q53907 streptomyce
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09zng8 helicobacte
09pj52 campylobact
094e25 oryza sativ
07403 prococcus
004807 perilla fru
09brk3 homo sapien
                       059516 pyrococcus
09y2r7 homo sapien
096rt2 homo sapien
027202 tetrahymena
09vaz2 drosophila
                                                                                       Q9ayy3 bacteriopha
Q92r09 rhizobium m
P57534 buchnera ap
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Q9epn2 mus musculu
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09k7l3 bacillus ha
P70928 bacillus li
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Q59022 methanococc
Q91jb4 arabidopsis
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Q9zvh5 arabidopsis
039489 bovine ephe
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09krk9 vibrio chol
               Q9myt3 oryctolagus
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29utb9 schizosacch
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09vdm0 drosophila
P71126 campylobact
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA49G10.1 (SIMILAR TO BOVINE SALIVARY PROTEIN BSP30).
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                       059516
09Y2R7
096RT2
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Q97G00
Q9Z7C3
Q9JRY0
Q03187
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Q9UWQ9
Q9C2G5
Q92X04
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092MG8
09PJ52
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09DD14
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09V6U5
09CNA1
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0978D9
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Q94FX0
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Q96KC3
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"A member of the PSP/plunc family of BPI proteins is expressed in the human parotid gland.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL. AF432917; AALZ8113.1; -. SEQUENCE 249 AA; 27110 MW; FD54B624A1A4CA7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ISLSELDKHSQ11NKFVNSVINTLKSTVSSLLQKEICPLIRIFIHHHHHHHHHHHHHHHHHH
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.
                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                          EMBL; AL121901; CAC03546.1; -. SEQUENCE 249 AA; 27011 MW; E64E0794A1B4DB7D CRC64;
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TISSUE=PAROTID;
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Haigh B.J., Wilkins R.J., Wheeler T.T.;
"The cloning and sequencing of two coNess coding for alternate forms of BEP30, a bowine member of the Parotid Secretory Protein family.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The cloning and sequencing of two cDNAs coding for alternate forms of BSP30, a bovine member of the Parctid Secretory Protein family."; Submitted (NOV-1966) to the EMBL/GenBank/DDBJ databases. EMBL; U79414; AAB38283.1;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                            121 KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.0%; Score 10; DB 6; Length 243; Best Local Similarity 100.0%; Pred. No. 0.097; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 10; DB 6; Length 240;
100.0%; Pred. No. 0.096;
ive 0; Mismatches 0; Indels
26513 MW; 850611DE9E43E358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U79413; AAB38282.1; -
SEQUENCE 243 AA; 26877 MW; 0C2D8DD45660E11C CRC64;
                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haigh B.J., Wilkins R.J., Wheeler T.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel, 03, Created)
01-MAY-1997 (TrEMBLrel, 03, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECIMINARY;
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QLWKLVLLCG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                               P79125
P79125;
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P79124;
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336 KLVLLCGV 343
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                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota: Neoptora; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCB1_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
"Arabidopsis CDNA clones.";
                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Phouanenavong S., Wan K., Submitted (OCT-201) to the EMBL/GenBank/DDBJ databases.

EMBL; AY060860: AAL28408.1; - 6841E96F24119670 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

3.2%; Score 8; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF367332. AAK32919.1;
InterPro; IPR002453; Beta_tubulin.
InterPro; IPR003017; Tubulin.
InterPro; IPR003008; Tubulin.FtsZ.
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 AA; 39251 MW; 2100EE72FCF9F96D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                      Last sequence update)
Last annotation update)
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PROSITE; PS00227; TUBULIN; UNKNOWN_1.
PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%; Score 8; DB 10
100.0%; Pred. No. 15;
tive 0; Mismatches
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                        01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 100.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G. Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Buck J., Broketal P., Brottier P.,
Borkova D., Botchan M.R., Buuck J., Broketal P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A de Pablos B., Delcher A., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; NCB1_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                          Lyne M., Rajandream M.A., Barrell B.G., Badcock K., Churcher C.M.:
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AL022334; CAA18408.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50048 MW; C395CB5D16C6AE5B CRC64;
                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
CG15015 PROTEIN.
                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last. sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 50.0 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.2%; Score 8; DB 3 Best Local Similarity 100.0%; Pred. No. 18; Matches 8; Conservative 0; Mismatches
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PRT;
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MEDLINE~20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002885; PPR.
Pfam; PF01535; PPR; 1.
Hypothetical protein.
SEQUENCE 432 AA; 50048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                        Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                  SPBC18H10.11C.
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Heiman T.J., Weil M.H., Libegwam C.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B. McIntosh T.C., McCod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Schael Kiamos I., Sinngson M., Scheeler F., Sinh H.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Wang X.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Wang X.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Wang X.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Wang X.,
RA Williams S.M., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Venter E., Zhu X., Smith H.O.,
REMB., AEDONGSTEL A., Wall M., Wolley R., Sull S., The genome sequence of Drosophila melanogaster.",
REMB., AEDONGSTEL A., RANGESTEL A.,
REMB., REDANGSTEL A.,
REMB., AEDONGSTEL A.,
REMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2%; Score 8; DB 4; Length 562; 100.0%; Pred. No. 23; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC001756; AAH01756.1; --
SEQUENCE 562 AA: 61370 MW; 8DD05DF242A6F5B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50002; SH3; 1.
SEQUENCE 525 AA; 58543 MW; 1CE378D9295B64E7 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred No. 22; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00326; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHOGLUCOMUTASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 LEKLKVDL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 LKVDLGVL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 LEKLKVDL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 LKVDLGVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            096740
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ID 05
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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Ekkunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Ekkunishi Y., Konno H., Adachi J., Fukuda S., Alicawa M., Nishi K., Kisosawa H., Kondo S., Yamanaka I., Asato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Pesole G., Quackenbush J., Sakani K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Loons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Anderia M., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Mashima M., Matshaw-Bonis A., Yoshida K., Kawaji H., Kohtsuki S., A., Washiyaw-Boris A., Yoshida K., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam J.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
                                                                                                                                    Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodenlia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.2%; Score 8; DB 11; Length 562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00710; PGM_PMM; 1.
SEQUENCE 562 AA; 61418 MW; 37854F785A24F71C CRC64;
             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
2610020G18RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
METHYL-ACCEPTING CHEMOTAXIS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    706 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                        MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1919407; 2610020G18Rik.
                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; T1SSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK011485; BAB27648.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.2%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00509; PGMPMM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001485;
                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00949; 3PMG.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 LKVDLGVL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 LKVDLGVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                    2610020G18RIK.
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McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Khabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                    "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8; DB 5; Length 720;
Pred. No. 29;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White S.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76965 MW; 8C13631C45F769E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018 (1998).
EMBL: 2810:20; CABO4106.2; -
SEQUENCE 720 AA: 81002 MW; FC53702AB0D381B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-A0G-1998 (TrEMBLrel. 07, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9KNF1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MALTODEXTRIN PHOSPHORYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 28;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             817 AA
                                                                                                                                                                                                                                                                                                                InterPro; IPR004089; Chemotaxis_transducer.
InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Scor
v 100.0%; Pred
0; M
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                                                                                                                                                                                     Nature 406:477-483(2000).
EMBL; AE004261; AAF95007.1; -.
HSSP; P02942; 1QU7.
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.2°
Best Local Similarity 100°
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00672; HAMP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 706 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 STVSSLLQ 213
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286 EAEKLLNN 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 EAEKLLNN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F14B6.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  062162; 0903J4;
                                                                                                                                                                                                                                                                                        TIGR; VC1859;
                                                                                                                                                      cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White
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Q9KNF1
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SEQUENCE FROM N.A.
STRAILM-EL TOR NISSEL / SERCHYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnollophyta: eudicotyledoms; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. D'Ampage M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W., D'Ampage M., Vezzi A., Mayer K.F.X., Quetier F., Salanoubat M.; Studmitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%; Score 8; DB 16; Length 817; 100.0%; Pred. No. 32; 1:ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 817 Aa; 92565 MW; 253B612226AD722E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 895 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000811; Phosphorylase.
Pfam; PF00343; phosphorylase; 1.
PROSITE; PS00102; PHOSPHORYLASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0107; PROTEIN KINASE_ATP; 1.
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.";
Nature 406:477-483(2000).
EMBL; AE004345; AAF95927.1; -.
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les 8; Conservative
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SMART; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00490; 2ECP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_Tax1D=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                     cholerae
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RA Addams M.D., Celligers S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celligers S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celligers S.E., Holt R.A., Bashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Chango M., Mikhos G.L.G.,
RA Man K.H., Doyle C. Baxter E.G., Helt G., Change M., Mikhos G.L.G.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis R.C., Bucam D.A., Buller H., Caddeu E., Center A., Chandra I.,
RA Grablos B., Delchar M.P., Deller S., Dulny P., Brottier P.,
RA Grablos B., Delchar M., Deller S., Dulny P., Brottier P., Bouse M., Doug L.E., Downes M., Dugan-Rocha S., Dulny P., Brottier P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Brits N.L., Harvey D., Heiman T.J., Hernandez J., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Weir M.-H., Ling Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., J., Wai M.-H., J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Moshrefi A.,
RA Related B., Minton N.Y., Streng R., Pacled J.W., Resee M. G.,
Spier E., Spradling A.C., Stapleton M., Strong R., Pacled J.W.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Jeng Z.Y., Wassaraman D.A., Weilsenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H. Schener R., Wang Z.Y., Wassaraman D.A., Weilsenbach J.,
RA Jeng C., Staveri J.S., Zhan M., Zano Q., Zheng G., Zhen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                            0; Gaps
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                          3.2%; Score 8; DB 10; Length 895; 100.0%; Pred. No. 35; 0; Indels ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                    895 AA; 98180 MW; 186BD5BB5F0B9DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                             Local Similarity
es 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 CGVLTGTS 319
                                                                                                                                                                                                                                                                                                                                                                                                              11 CGVLTGTS 18
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                                                                                                                 Transferase.
                                                                                                                                                    SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                         DB 5; Length 1419;
                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:16737) (PROTEIN FOR MGC:19613).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                  1419 AA; 158585 MW; 4719061A0FC5A2C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 7; DB 4; Length 74;
100.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine ephemeral fever virus (BEFV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Ephemerovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                     InterPro; IPR000572; EUK_OXidored_molyb.
InterPro; IPR003651; FN_III.
InterPro; IPR003651; FN_III.
InterPro; IPR00367; TYR_phosphatase.
InterPro; IPR00342; TYR_phosphatase.
Pfam; PF0041; fn3; 2.
PRINTS; PR00041; fn3; 2.
PRNTS; PR000700; PRTYPHPHTASE.
SMART; SM00060; FN3; 2.
PROSITE; PS00559; MOLYBDOPHATASE_1; I.
PROSITE; PS00363; TYR_PHOSPHATASE_1; I.
PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
                                                                                                                                                                                                                                                                                                                                                                                          74 AA.
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                                                                                                                                                                                                                                                      ; Pred. No. 53; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN, NEUROBLASTOMA, AND MELANOMA;
                                                                                                                                                                                                                                         3.2%; Score 8;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                           PKT;
           FlyBase; FBgn0034085; CG18243
                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
8; Conservative
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Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                            205 KSTVSSLL 212
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606;
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                                                                                                                                                                                     Hydrolase.
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      096A10;
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039489
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Matches
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O
                   McWilliam S.M., Kongsuwan K., Cowley J.A., Byrne K.A., Walker P.J.;
"Genome organization and transcription strategy in the complex GNS-L
intergenic region of bovine ephemeral fever rhabdovirus.";
J. Gen. Virol. 78:1309-1317(1997)
EMBL: U72399; AAB63108 1;
SEQUENCE 107 AA: 12219 MW; 4BB2DFBBA0E11709 CRC64;
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE: TISSUE-HEART;
Sayeed R.A., Grace A.A., Vandenberg J.I.;
"Immediate-early gene response to acute pressure-overload in the rabbit heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;0
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DHAND BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR (FRAGMENT).
                                                                                                                                                                                                                                      Query Match 2.8%; Score 7; DB 12; Length 107; Best Local Similarity 100.0%; Pred. No. 55; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.8%; Score 7; DB 6; Length 136; Best Local Similarity 100.0%; Pred. No. 68; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rabbit heart.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ291300, CAB94840.1;
HSSP; P22415; 1AN4.
InterPro; IPR001092; HUH_dim.
PRam; PP00010; HUH; 1.
SMART; SM00353; HLH; 1.
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NON_TER 136 136
SEQUENCE 136 AA; 14913 MW; 006512C46A6E0DD6 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 14.5 KDA PROTEIN PH1841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=97335257; PubMed=9191923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikoshii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               142 QIINLKA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 LKSTVSS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 LKSTVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                  11 QIINLKA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  059516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MYT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9MYT3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 19
059516
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakasawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kiuchi H., "Complete Sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G., Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W., Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.; "Cloring and functional analysis of CDNAs With open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 141; . 70;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 7; DB 4; Length 171;
100.0%; Pred. No. 83;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem/progenitor cells.";
Genome Res. 10:1546-1560(2000).
EMBL: AF077037, AAD27770.1;
InterPro: JRF000561; EGF-like.
SMART; SM00181; EGF, 1.
PROSITE: PS00022; EGF_l; UNKNOWN_1.
PROSITE: PS01865: EGF_l; UNKNOWN_1.
EGF-like domain; Clycoprotein.
SEQUENCE 171 AA; 18597 MM; 91A42CD2B2CB0883 CRC64;
                                                                                                                                                                                                                      EMBL, AP000007; BAA.0962.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 141 AA; 14480 MW; 6834B298F6879922 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 7; DB 1
100.0%; Pred. No. 70;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20499367; PubMed=11042152;
                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.0
اندم 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                      DNA Res. 5:55-76(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 PTS1SLS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 TQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 PTSISLS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 TOLOTLI 65
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Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota, Neopuera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN B, STRAIN B, L.A. LOCKSHIN C., Orlas E.; Lockshin C., Orlas E.; "Nucleotide sequence of the cDNA encoding a mating-related gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
O
                                                                                                                                                                                      DB 4; Length 171; 5. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 181;
                                                        SEQUENCE FROM N.A.

Yang Y.C., Chen S.Y., Chang M.S.;

"Cloning and characterization of p18.";

"Cloninted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF275744; AAK69412.1; -.

SEQUENCE 171 AA; 18567 MW; 81A52CD2B2CB0883 CRC64;
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terrahymena thermophila.";
Submitted (JUL-1970) to the EMBL/GenBank/DDBJ databases.
EMBL; X53088; CAX3734.1;
SEQUENCE 181 AA: 19813 MW; 97711EC2F76113D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) INITIATION AND CO-STIMULATION FACTOR-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%; Score 7; DB 5; Best Local Similarity 100.0%; Pred. No. 88; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              181 AA.
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                      2.8%; Score 7; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBL.rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                  100.08;
                                                                                                                                                                    Query Match
Best Local Similarity 100...
For 7; Conservative
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                 243 TQLQTLI 249
                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                              59 TQLQTLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG12426 PROTÈIN.
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen, L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Clampe M., Pfeiffer B.D.,

RA Brail J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Rallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Rabrill J.F., Apbayani A., An H.-J., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Rabris W., Cawley S., Dahlke C., Dowenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Pleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Pleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Pleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Pleischmann W.,

RA Bortis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Jalai M., Kalush F., Karpen G.H., Wei M. H., Libayam C., Lai Z.,

RA Jalai M., Moy M., Murphy B., Murphy L., Muzny D.M., Netson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Netson D.L.,

RA Reinert K., Remington K.S., Jana S., Pollard J., Puri V., Resee M. G.,

RA Spier E., Spradling A.C., Sanders R.D., Smith T.,

RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Savari J.S., Zhan M., Zhang S., Zhu X., Smith H.O.,

RA Sheng S.M., Woodage T., Wolfor S., Zhu S., Zhu X., Smith H.O.,

RA Shong S.M., Woodage T., Worter J.C.;

RA Sheng S.M., Rassarman D.A., Weinsenbach J.,

RA Jaben S.A., Whyers E.W., Rubin G.M., Venter J.C.;

RA Jaben S.A., Whyers E.W., Rubin G.M., Venter J.C.;

RA Jaben S.A., Markin R.D., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of a gene encoding 22 kDa functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage MB78 (Salmonella typhimurium bacteriophage MB78).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 7; DB 9; Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein of Bacteriophage MB78.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF349435; AAK30159.1;
SEQUENCE 195 AA: 22353 MW; 09FF20ECF44B6444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 AA; 20357 MW; C776041F8CC05B39 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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o. 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.08; Pred. No. 90;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase, FBgn0039552; CG12426.
SEQUENCE 187 AA; 20357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003762; AAF56754.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gupta L., Chakravorty M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=52971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 LLTAVTI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LLTAVT1 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Pfam; PF01872; RibD_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE COLICIN V PRODUCTION HOMOLOG TRANSEMBRANE PROTEIN.
Rhizobium mellloti (Sinorhizobium mellloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
KRizobiaceae; Sinorhizobium.
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                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                   199 AA.
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  ), Pred. No. 94;
0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                 PRT;
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MEDLINE=20445173; PubMed=10993077;
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InterPro; IPR002734; Ribb_C.
100.08;
  Best Local Similarity 100.
Matches 7; Conservative
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Nature 407:81-86(2000).
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SEQUENCE 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=118099;
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                                                                           148 ASLDLLT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 LLDNLGN 150
                                                                                                                        38 ASLDLLT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LLDNLGN 27
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Q92R09
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                                                                                                                                                                                          Gaps
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Zhu F., Yan W., Chai Y.B., Shao C., Peng W.D., Yang A.G., Wang C.J.,
Zhao Z.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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NCBL_TaxID=111955;
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                                                                                                                       Query Match 2.8%; Score 7; DB 16; Length 207; Best Local Similarity 100.0%; Pred. No. 99; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.8%; Score 7; DB 4; Length 208; Best Local Similarity 100.0%; Pred. No. 99; Matches 7; Conservative 0; Mismatches 0; Indels
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Crenarchaeon, Sulfolobus tokodaii strain?.";
DNA Res. 8:123-140(2001).
EMBL: AP000982: BAB65389.1; --
Hypothetical protein; Complete proteome.
                                                                                                                                                                                   0; Indels
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Oxidoreductase: Complete proteome.
SEQUENCE 207 AA: 23942 MW: DAC973284089D76A CRC64;
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SEQUENCE 208 AA; 22687 MW; CD4C5723C62CAF6F CRC64;
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01-NoV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLEEL. 19, Last Sequence update)
01-DEC-2001 (TrEMBLEEL. 19, Last annotation update)
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PubMed=11572479;
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                                                                                                                                                                                                                                            102 LKISNSL 108
                                                                                                                                                                                                                                                                                                     178 LKISNSL 184
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Query Match
Best Local Similarity
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                                                 8 VLLCGVL 14
                                                                        9 VLLCGVL 15
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                                                           0; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Eukaryota; Metazoa: Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banerjee G., DePonte K., Marcantonio N., Kantor F.S.,
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EMBL; AF209922: A8457825.1; -. SEQUENCE 222 AA; 25368 MW; 4DIA6062763FEECO CRC64;
                                2.8%; Score 7; DB 17; Length 212; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.8%; Score 7; DB 11; Length 217; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ131846; CAC20671.1; -.
HSSP; P36956; 1AM9.
212 AA; 23346 MW; EFAD7B9E11606323 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update
                                                                                                                                                                      217 AA
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                                                          U; Mismatches
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Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                           Conservative
                                                                                                                                                                      PRELIMINARY;
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                                             Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                 102 LKISNSL 108
                                                                                                         188 LKISNSL 194
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Fikrig E.;
SEQUENCE
                                    Query Match
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                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
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2.8%; Score 7; DB 5; Length 222; 100.0%; Pred. No. 1.1e+02; ative 0; Mismatches 0; Indels
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SMART; SM00101; EGF; I.:
FROSTIE: PS00022; EGF_I; UNKNOWN I.
SEQUENCE: 223 AA; 23867 MW; A85E:A03C7DD2C16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last.sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0610007C21R1K PROTEIN.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:13322).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                           223 AA.
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Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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MBL; AK002276; BAB21981.1; ...
MGD; MGI:19818; 0610007621Rik.
InterPro; IPR000561; EGF-11ke.
                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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Pfam: PF00702; Hydrolase; 1. SEQUENCE 232 AA; 24854 MW; 7A977F7A550DBF15 CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-21201076; Pubmed-11278540;
Yu T.-W., Mueller R., Mueller M., Zhang X., Draeger G., Kim C.-G.,
Leistrer E., Floss H.G.;
"Mutational analysis and reconstituted expression of the biosynthetic
genes involved in the formation of 3-amino-5-hydroxybenzoic acid, the
starter unit of rifamycin biosynthesis in Amycolatopsis mediterranel
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Blosynthesis of the ansamycin antibiotic rifamycin: deductions from
the molecular analysis of the rif biosynthetic gene cluster of
Amycolatopsis mediterranei 5699.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim C.G., Yu T.W., Fryhle C.B., Handa S., Floss H.G.; "3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the formation of the precursor of mC?N units in ritamycin and related antibionics."
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                             Query Match 2.8%; Score 7; DB 4; Length 229; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC011006; AAH11006.1; -.
SEQUENCE 229 AA: 24688 MW: F2C63F934A47ED33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floss H.G.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AFG40570; AAC01721.1; -.
InterPro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amycolatopsis mediterranei (Nocardia mediterranei).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 276:12546-12555(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98174059; PubMed=9512878;
                                                                       SEQUENCE FROM N.A.
TISSUE=BRAIN, AND GLIOBLASTOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. Biol. 5:69-79(1998).
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                                                                                                                                                                                                                                                                                   243 TQLQTLI 249
                                                                                                                                                                                                                                                                                                                  117 TOLOTLI 123
                                                                                                            Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHATASE.
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Mirels L., Ball W.D.;
"Neonatal rat submandibular gland protein SMG-A and parotid secretroy
protein are alternatively regulated members of a salivary protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean).

Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I: Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
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                                                                     Gaps
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NEONATAL SUBMANDIBULAR GLAND PROTEIN.
0B36EC779025986E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 7; DB 11; Length 235; 100.0%; Pred. No. 1.1e+02;
DB 2; Length 232;
0, 1.1e+02;
ches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEONATAL SUBMANDIBULAR GLAND PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SUBMANDIBULAR GLAND;
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Query Match 2.8%; Score 7; DB 2 Best Local Similarity 100.0%; Pred. No. 1.1 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.1.
Amservative 0: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multigene family.";
J. Biol. Chem. 267:2679-2687(1992).
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EMBL; M83209; AAC06334.1; -.
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SEQUENCE 235 AA; 24529 MW;
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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                                                                                                                                                                                              129 SLLDNLG 135
                                                                                                                                20 SLLDNLG 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mirels L.,
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InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Trypsin.
                                                                                       EMBL; AF130865; AAD29675.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium acetobutylicum.
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Best Local Similarity luo...
7; Conservative
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                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 7; Conserv
                                                                            TRYPSIN FAMILY
                                                                                                                 MEROPS; S01.103;
                                                                                                                                                                                                                                                                                                                                  131 ANVTVAG 137
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLIND=21295560; PubMed=11402195; Davis S.J., Bhoo S.H., Durskl A.M., Walker J.M., Vierstra R.D.; Jabovis S.J., Bhoo S.H., Durskl A.M., Walker J.M., Vierstra R.D.; "The heme-oxygenase family required for phytochrome chromophore blosynthesis is necessary for proper photomorphogenesis in higher
                                                           biosynthesis is necessary for proper photomorphogenesis in higher
                                                                                                                                                                                        0;
                     MEDLINE=21295560, PubMed=11402195;
Davis S.J., Bhoo S.H., Durski A.M., Walker J.M., Vierstra R.D.;
"The heme-oxygenase family required for phytochrome chromophore
                                                                                                                                                            2.8%; Score 7; DB 10; Length 249; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 7; DB 10; Length 250; 00.0%; Pred. No. 1.2e+02; ve 0; Mismatches 0; Indels
                                                                                                                                                                                     0; Indels
                                                                                                           NON_TER 1 1 203BE0A22C455E22 CRC64; SEQUENCE 249 Aa; 28319 MW; 203BE0A22C455E22 CRC64;
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                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Plant Physiol, 126:656-669(2001).
                                                                                   Plant Physiol, 126:656-669(2001).
EMBL, AF320025; AAK63009.1; ...
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                                                                                                                                                                        Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                             Glycine max (Soybean)
          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     185 AEKLLNN 191
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                                                                                                                                                                                                               81 AEKLLNN 87
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SEQUENCE
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Screen S.E., St Leger R.J.;
"Isolation of multiple protease genes from the entomopathogenic fungus "Esolation of multiple protease genes from the entomopathogenic fungus Metarhizium anisopliae.";
Submitted (FEB-1999) to the EMBI/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov W.L., Sabathe F., Douette-Stamm L., Soucaille P., Daly M.J., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

EMBL, AE007755, AAX80523-1;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PREDICTED S-ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8%; Score 7; DB 3; Length 255; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88DD979ED300E4B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 7; DB 100.0%; Pred. No. 1.2vtive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00202; Tryp_SFS: 1.
PROSITE: PS50240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS: UNKNOMN_1.
PROSITE: PS00135; TRYPSIN_SER; 1.
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SEQUENCE 255 AA: 26289 MW; 88DD97
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InterPro; IPR001601; Meth-transf.
InterPro; IPR000051; SAM_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; Comparative genomes of Chlanydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                            Chlamydia pneumoniae (Chlamydophila pneumoniae).
                              262 AA
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Best Local Similarity 100.0%; Pred. No. 1.2
Matches 7; Conservative 0; Mismatches
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                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 10, 01-JUN-2001 (TREMBLRel. 17, CT598 HYPOTHETICAL PROTEIN.
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                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CWL029;
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                                                                                                                                                                                                                                                           Bacteria;
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0927C3
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2.8%; Score 7; DB 16; Length 262;

Query Match

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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrell B., Rajandream M.A.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; Z46255; CAA86348.1; -.
InterPro; IPR002114; PTS_HPr_ser.
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SEQUENCE 267 AA; 28771 MW; ACA79F341A4319FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHROMOSOME VI LAMBDA CLONE.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ZK1086.3 PROTEIN
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  267 AA.
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Science 28:2010-2018(1998).
EMBL; 270269; CAA94222.1; -.
Interpro: IPRO02485; DuF13.
Probom; PRO1482; DuF13; 1.
                                Conservative
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
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                                                                                            242 KTOLOTL 248
                                                                                                                                                    132 KTQLQTL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Churcher C.;
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PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
SEQUENCE 295 AA; 31582 MW; 82C853BBDE
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RA Addms M.D. Celnister S.E. Li P.W. Hoskins R.A. Galle R.F.,

Ranantides P.G., Scherer S.E. Li P.W. Hoskins R.A. Galle R.F.,

George R.A. Lewis S. Scherer S.E. Li P.W. Hoskins R.A. Galle R.F.,

Randon R.C., Rogers Y.H.C., Blazej R.G., Changen D.D.,

RA Brita J.F. Apbayani A. An H.-J. Andrews Pfannkoch C. Baldwin D.

Ballew R.M. Basu A., Baxendale J. Bayraktaroglu L. Beasley E.M.,

Ballew R.M. Boschan M.R. Boack J. Bayraktaroglu L. Beasley E.M.,

RA Burtis R.C., Busam D.A., Lewissel D., Bhandari D., Bolshakov S.,

RA Burkova D., Borchan M.R., Boack J., Bayraktaroglu L., Beasley E.M.,

RA Burtis R.C., Busam D.A., Dallew C., Davenport L.B., Davies P.,

RA Cerry J.M., Gawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Dowers M., Dayan-Rocha S., Dunkoy B.C.,

Burtis R.C., Gabrielisa C.C., Ferraz C., Ferriar S., Fleischman M.,

RA Botlon D., Houston K.A., Howland T.J., Hernandez J.R., Black S.,

All M. Malshina A.E., Garg N.S., Gelbart W.M., Glasser K.,

All M. Malshina A.E., Karpen G.H., J., Mei M.-H., Iberwam C.,

Jakop P., Lei Y., Karleh F., Karpen G.H., J., Mei M.-H., Iberwam C.,

Allali M., Kalish F., Karpen G.H., Moshrefi A.,

Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Bazzolo D.R., Motlonsh T.C., Merker S., Wang D.H., Wang X.,

RA Bazzolo D.R., Motlonsh T.C., Stapleton M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Wang Z.-Y. Wassanman D.A., Weinsten E., Wang A.H., Wang X.,

Wang Z.-Y. Wassanman D.A., Weinsten E., Wang A.H., Wang X.,

Wang Z.-Y. Wassanman D.A., Weinsten S., Zhu X., Smith H.O.,

Raben R. Schoel R. W., Rubin G.M., Venter J.C.,

Raben R. Schoel R. W., Rubin G.M., Venter J.C.,

Raben R. Schoel R. W., Rubin G.M., Venter J.C.,

Raben R. Schoel R. Schoel R. W., Rubin G.M., Venter J.C.,

Raben R. Schoel R. Schoel R. W., Rubin G.M., Venter J.C.,

Raben R. 
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                Gaps
                                                                                              .,
                                                  2.8%; Score 7; DB 5; Length 290; 100.0%; Pred. No. 1.3e+02; Live 0; Mismatches 0; Indels
SEQUENCE 290 AA; 33362 MW; 80B56303FBCF4D6F CRC64;
                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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InterPro; IPR001753; Enoyl_CoA_hydrtse.
Pfam; PF00378; ECH; 1.
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; Pubmed=10731132;
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                                                                                            Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
                                    Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                  142 ILEKLKV 148
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NCBI_TaxID=7227;
                                                                                                                              54 ILEKLKV 60
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"Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. US. A. 98:3460-3465(2001).
EMBL, AE006088, AAKO2617.1; -...
InterProc. IPR000022: Polyprenyl_synt.
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Bacteria: Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 7; DB 16; Length 295; 100.0%; Pred. No. 1.4e+02;
                                                        2.8%; Score 7; DB 5; Length 295; 100.0%; Pred. No. 1.4e+02;
                                                                                          0; Indels
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les 0; Indels
82C853BBDEF705B9 CRC64;
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                                                                                                                                                                                                                                                                                                                      17, Last sequence update)
19, Last annotation update)
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11-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBOSE TRANSPORT ATP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
EMBL: AF010496; Acc16211.1;
InterPro: IPR003593; AAA.
InterPro: IPR003439; ABC_transportr.
                                                              100.0%; Pred. ...
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PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel, 17, Created)
01-JUN-2001 (TrEMBLrel, 17, Last sequent
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                                                                                            Conservative
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                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                      |-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella multocida.
                                                                      Best Local Similarity
Matches 7; Conserv
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Matches 7; Conserv
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SEQUENCE 295 AA;
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                                                                                                                                                                    205 AOEAEKL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AKQKAQE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_TaxID=1061;
                                                                                                                              78 AQEAEKL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_Tax1D=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AKUKAQE 80
                                                                                                                                                                                                                                                                                                                                                                          ISPA OR PM0533,
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                                                          Query Match
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STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031;
MEDLINE=20570466; PubMed=11121031;
MEDLINE=20570466; PubMed=11121031;
Mawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fabret C., Quentin Y., Chapal N., Guiseppi A., Halech J., Denizot F., Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                      2.8%; Score 7; DB 2; Length 305; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
                                                                                        ATP-binding.
SEOUENCE 305 AA; 32914 MW; D5AD58A707E922E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
CE 314 AA; 35061 MW; 2DA07090F36892ED CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 37.3 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
EMBL; AP000996; BAB60620.1; ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORMATE HYDROGENLYASE SUBUNIT 5.
InterPro; IPR001687; ATP_GTP_A. Pfam; PF00005; ABC_tran; 1. SMART; SMO0382; AAA; 1.
                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                    108 LILDVKA 114
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193 LILDVKA 199
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A Kunst F., Ogasawara N., Maszer I., Albertini A.M., Alloni G.,

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Bornise K., Bourster L., Brans A., Braun M., Brighell S.C., Bron S.,

RA Brouillet S., Bruschi C.W., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Chia S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chia S.K., Claser P., Goffeau A., Gollghtly E.J., Grandl G.,

RA Fitz C., Fijita M., Fujita Y., Fuma S., Calizzi A., Galleron N.,

RA Ghims S.Y., Glaser P., Goffeau A., Gollghtly E.J., Grandl G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Horn W., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Reyonolds S.,

RA Fleger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Freger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A.,

Vani A., Wambutt R., Wedler E., Wedler F., Vassarotti A.,

Vani A., Wambutt R., Wedler E., Wedler H., Weitzeneger T.,

Winters P., Wilpat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Ra The complete genome sequence of the gram-positive bacterium Bacillus

RT The complete genome sequence of the gram-positive bacterium Bacillus
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z71928; CAA96483.1; -.
                                                        Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 322 AA; 37274 MW; CEOBIFF05A498E73 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NIFE HYDROGENASE BETA SUBUNIT.
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0;
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Denizot F.C.;
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          Rakhely G., Zhou Z.Z., Adams M.W.W., Kovacs K.L.;
"Biochemical and molecular characterization of the [NiFe] hydrogenase from the hyperthermophilic archaeon, Thermococcus litoralis.";
Eur. J. Biochem. 266:1158-1156(1999).
EMBL: AF039208; AAB94933.1; -.
InterPro: JPR001450; 4Fe4S_ferredoxin.
Pfam, PF00037; fer4.
PROSTE: PS00198; 4Fe4S_FERREDOXIN; 2.
SEQUENCE 369 AA: 43293 MW; 42332FFB7D749973 CRC64;
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Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                    Query Match 2.8%; Score 7; DB 1; Length 369; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.8%, Score 7: 10B 3; Length 473; Best Local Similarity 100.08; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL513443; CAC28680.1; -.
Hypothetical protein.
SEQUENCE 373 AA, 40973 MW; 7A9704F940E22DB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 41.0 KDA PROTEIN.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Plasmid pSymB (megaplasmid 2).
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MEDLINE=20050631; PubMed-10583413;
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                                                                                                                                                                                                                                                                         98 DIFGLKI 104
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NCBI_TaxID=382;
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Job time: 212 sec
        MEDLINE=21396508; PubMed-11481431;
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Human serreted pro
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Novel human diagno
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Rat dHAND protein
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B. lactofermentum
Thrombomucin, Uni
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Human polypeptide
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AAM96148
ABB38333
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ABG19852
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AAU19282
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  AAW69221
ID AAW6
XX
 RESULT
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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938.811 Million cell updates/sec
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Human parotid secr
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Human brain expres
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Novel human diagno
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                                                                                                                                                   249
1 MLOLWKLVLLCGVLTGTSES.....NVIQQVVDNPOHKTQLQTLI 249
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                             747574 seqs, 111073796 residues
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                                                              protein search, using sw model
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ABB41435
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AAM75111
AAM35227
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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amplification or immuno assays), particularly for diagnosis of digestive, non-immune defensive, endocrine or immune system disorders. A particular application is diagnosis of cancers of the salivary gland, thymus and pancreas which are associated with high levels of hSSP. The protein is also useful as antifungal, antibacterial, antiparasitic and antiviral expressing it, are used in screening tests to identify specific (ant)agonists, e.g. antibodies (Ab), polypeptides and antisense nucleic acids, which are potentially useful for treating conditions associated with excessive hPSP production. Cells containing the DNA are used to express the recombinant production and this can be used to raise Ab, useful for diagnosis, therapy, for affinity purification and to identify
                                                                                                                                                                                                          Parotid secretory protein; hPSP; digestive disorder; endocrine disorder; non-immune defensive disorder; immune system disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention. The hPSP DNA is useful for chromosome identification and isolation of the corresponding genomic DNA. The DNA and protein can be used to detect abnormal levels of hPSP (in standard blotting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the human parotid secretory protein (hPSP) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding human parotid secretory protein or its fragments - useful for diagnosis and treatment of, e.g. digestive and endocrine disorders and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 249; DB 19; Length 249; 100.0%; Pred. No. 2.6e-221; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature hPSP"
                                                                                                                                                                                                                                                                                                                                                                                                                     Jonation/Qualifiers
                                                                                                                                          Human parotid secretory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.0%;
Matches 249; Conservative 0
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                                                                   16-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                              therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM;
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AAW69221;
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This represents a human parotid secretory protein (HPSP). Antagonists that bind specifically to, and modulate activity of HPSP are used to treat cancer and autoimmune diseases particularly of secretory or gastrointestinal tissue, e.g. cancer of salivary gland, thyroid, prostate, breast, gastroiditis, insulin-dependent diabetes, pancratitis, uscarative colitis, forbid sideses and atrophic gastritis. Host cells conteating vectors comprising the HPSP nucleic acid are used to produce recombinant HPSP which is used to generate antibodies and to screen for its antagonists. Antibodies are useful directly as antagonists, to transport drugs to HPSP-expressing cells, to detect cells that express HPSP to monitor patients being treated with HPSP may from natural sources. Expression of HPSP may colect the expression of HPSP from natural sources. Expression of HPSP may to detect HPSP-encoding sequences (optionally after amplification by PCR) by hybridiaation, particularly for diagnosis and monitoring of disease, but also for mapping the chromosomal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       secretory tissue; gastrointestinal tissue; HPSP, Sjorgen's syndrome; Graves disease; thyroiditis; insulin-dependent diabetes; pancreatitis; ulcerative colitis; Crohn's disease; atrophic gastritis.
                                                       121 kglmlsfpvtanvtvagpiigqiinlkas1d1ltavtietdpqthqpvavlgecasdpts 180
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                                 181 ISLSILLOKHSQIINKFVNSVINTIKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ
                                                                                                                                                                                                                                                                                                                                                                                           Parotid secretory protein; human; cancer; autoimmune disease;
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                                                                                                                                                                                                                                        AAW60682 standard; Protein; 249 AA.
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                                                                                                            181 ISLSLLDKHSQ11NKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ 240
                                                                                                                                                 Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
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                              1 MLQLWKLVLLCGVLTGTSFSLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60
                                                                                                                                                                                                                                                                                                                                          proliferation; tumourigenesis; identification; cancer; cytostatic; mootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiaquiqqenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; tromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated antibody that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker KP, Goddard A, Gurney AL, Hillan KJ,
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment, diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                              Human PRO1025 protein sequence SEQ ID NO:38.
Mismatches
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99WO-US12252.
99US-0141037.
99US-0143048.
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Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1999;
                                                                                                                                                                                                                                                                                           29-JAN-2001
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those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gilal, astrocytal, hypothalanic and other glandular, macrophagal, epithelial, strocytal, hypothalanic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AACS8345 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AACS8367 to AACS8367 and AAR24057 to AACS8467 thuman PRO PRO polynucleotide and protein sequences given in the exemplification of
one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO717, PRO809, PRO810, PRO848, PRO943, PRO1005, PRO1005, PRO1005, PRO1005, PRO1007, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO2181, PRO234, PRO34, PRO84, PRO3117, PRO1710, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the
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                                                                                                                                                                                                                                    treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
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Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, brain disorders, skeletal muscle disorders, eye disorders, cobesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease,
                                                                                                                                                                                                                                                                                  This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA8775-A8774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the sequence proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene
                                                                                                                                                                                                  Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dlgvlgkssawglakqkaqeaekllnnviskllptntdifglkisnslildvkaepiddq 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dementia, hyperlipidaemia, septic shock and impotence.
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100.0%; Pred. No. 2.6e-221;
tive 0; Mismatches 0;
                                                                                                                            Bougueleret L, Dumas J, Duclert A;
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                                                                                                                                                                                                                                                           Claim 9; Figure 10; 306pp; English.
                           99WO-1B02058
                                                       98US-0113686
                                                                   99US-0141032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 249; Conservative
                                                                                                                                                                                                                              mapping procedures -
                                                                                                                                                        2000-442637/38.
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                                                                                                                                                                    N-PSDB; AAA87727
                                                                                                 (GEST ) GENSET.
                                                       22-DEC-1998;
                           20-DEC-1999;
                                                                      25-JUN-1999;
29-JUN-2000
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Best Local S
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61 DLGVLQKSSAWQLAKQKAQEAEKI,LNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 49 Secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 249;
                                                                                                        Secreted protein; prevention; treatment; diagnosis; disease;
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100.0%; Pred. No. 2.6e-221;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 281; 307pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                            99US-0141032.
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                                                    Human secreted protein #10.
05-APR-2001 (first entry)
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Matches 249; Conservative
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                                                                                                                                 infection
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AMA2593. The proteins can have activities based on the internal proteins and have activities based on the insular activities based on the proteins can have activities based on the insular and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide, antiagetes; antiantegen; cardiant; antianaemic; antianaemic; antianaemic; antianaemic; cytostatic; neuroprotective; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; antidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; antidabetic; cytostatic; neuroprotective; antidaperson; nootropic; antidabetic; cytostatic; neuroprotective; and pending and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonitis or antigonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cancer, multible sclerosis, depression, allowed the protein and disperses of allowed partner's disease, neurodegenerative and
                                           antibacterial endocrine; cardiant, central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiangregant; haemostatic; vulnerary; antiuleer; osteopathic; eczema; dermatological; antialleryic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; immunostimulant; gene thorapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmulty; genetic disease; hematopoletic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
                                                                                                                                                                                                                                                                             thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
cancer; ulcer; HIV infection; human immunodeficiency virus;
                          antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated human polynucleotides encoding polypeptides, useful for treatment and diaynosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 260; 1217pp; English.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                            neurological disorder.
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260 AA;
 Sednence
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1 MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV 60 Length 260; Indels 53.8%; Score 134; DB 22; L 100.0%; Pred. No. 2.6e-115; tive 0; Mismatches 0; Conservative Similarity 134; Query Match Best Local S Matches

12 mlq1wklv1lcgv1tgtses1ldn1gnd1snvvdklepv1heg1etvdnt1kgi1ek1kv 71

qq

0; Gaps

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AAM62308 standard; Protein; 50 AA.

a

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measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
61 DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDDG 120
                Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                  Peptide #8941 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 34070; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 PIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTSISLSLLD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.1%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                       ABB41435 standard; Peptide; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0235359.
04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
                                                                                                                                                                                                                                  04-FEB-2002 (first entry)
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                                                                                           132 kginlsfpvtanvt 145
                                                             121 KGLNLSFPVTANVT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AA;
                                                                                                                                                                                                                                                                                                                                                             WO200157277-A2.
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
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                                                                                                                                                                                                      ABB41435;
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                                                                                                                                                        ABB41435
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AAM35227
$\text{SYN} \text{SYN} \text{SYN}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 34413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 35417.
                                                                                                                                                                             microarray, Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 34413; 650pp + Sequence Listing; English.
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                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 piiggiinlkasldlltavtietdpgthgpvavlgecasdptsislslld 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
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03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0235359.
04-OCT-2000; 2000GB-0024263.
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                                                                 05-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483446/52.
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Matches 50; Conserv
                                                                                                                                                                                                                                                                                                     WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               04 - FEB - 2000;
                                                                                                                                                                                                                                                        Homo sapiens
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                      AAM62308;
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δ
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #9264 encoded by prube for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 35417; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.1%; Score 50; DB 22;
100.0%; Pred. No. 1.6e-38
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                  Chen W, Rank DR;
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2000US-0234687.
2000US-0236359.
                                                                                                                                                                     26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
04-06-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                30-JAN-2001; 2001WO-US00668
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000GB-0024263
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Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 AA;
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WO200157276-A2.
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30-JUN-2000;
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27-SEP-2000;
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                                                  09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
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58 LKVDLGVL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB54100;
                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                Human genome-derived single exon nucleic acid probes useful for
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0
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                                                                                                                                                                                                                                                                                                                                                                   1 piiggiinlkasldlltavtietdpgthgpvavlgecasdptsislslld 50
                                                                                                                                                                                                                                                                                              Length 50;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                           1.6e-38;
                                                                                                                                                                                                                                                                                              20.1%; Score 50; DB 22;
                                                                                                 analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                       100.08; Pred. wc.
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                                                                                                                         Claim 27; SEQ ID No 35496; 654pp; English.
                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #20795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG20804 standard; Protein; 316 AA
(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                         50; Conservative
                                                                                                                                                                                                                          human genetic disorders.
                            Penn SG, Hanzel DK,
                                                       WPI: 2001-488897/53
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                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                     50 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                               Query Match
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for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGO0010-ABG30277 represent novel human
                                                                                                                                                                                                                                                                                                                       diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human: pancreas; pancreatic cancer; pancreatic cancer antigen; detection; dagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; issue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins, called pancreatic cancer antigens, given in AAB54008 to
AAB54466. The human pancreatic cancer antigens have cytos⊧atic,
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB54100 standard; Protein; 511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 316 AA;
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                                                                                                                                              Agonists and antagonists to the antigens can be screened for The pancreatic disorders, especially concernation to the antigens can be screened for The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestina) pulmonary, cardiovascular, renal or proliferative disorders. AAC99212 to AAC99240 and AAB6467 represent sequences used in the exemplification of the present invention.
neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, appraechlogical, cardiant and antihiflammarcry activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent explains of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
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5. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB70056 standard; Protein; 525 AA.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 lkvdlgvl 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                            specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome, synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
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                                                                                                                                                                                                             DB 22; Length 525;
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                                                                                                                                                                                                                                                 0; Indels
                                        (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatological; osteopathic; neuroprotectant.
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, Jen S, Carter D;
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                                                                                                                                                                                                                                 ; Pred. No. 65;
0; Mismatches
                                                                                                                                                                                                               3.2%; Score 8;
100.0%; Pred. No
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2002 (first entry)
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 8; Conservative
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                                          sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                      525 AA;
                                                                                                                                                                                                                                                                                                             349 lekikvdl 356
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                downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
specific for P. acnes proteins. These antibodies can be used to
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                                                                                                                                                                                                                                     3.2%; Score 8; DB 22; Length 601;
                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 40194.
                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                      100.0%; Pred. No. 74;
ative 0; Mismatches
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                 8; Conservative
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                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                601 AA;
                                                                                                                                                                                                                                                                                                                                                              263 piiggiin 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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                                                                                                                                                                                  Sednence
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Sequence 1419 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAX41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
                                                                                                                                                                                                                                                                                                 Human; secreted protein; fusion protein; gene therapy; protein therapy;
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                               Gaps
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R, Lafleur DW;
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Length 1419;
                             0; Indels
                                                                                                                                                                                                                                                                     Human secreted protein encoded by gene 85 clone HSDGN55.
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A, Duan RD, Kyaw H, Ebner R,
                Pred. No. 1.6e+02;
3.2%; Score 8; DB 22;
    100.0%; Preq. ...
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                                                                                                                                                                        AAY41392 standard; Protein; 43 AA.
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98US-0080313.
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                             Conservative
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Best Local Similarity
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                                                           205 KSTVSSLL 212
                                                                               644 kstvssll 651
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01-APR-1998;
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                                                                                                                                          RESULT 16
                             Matches
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conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in (see AAZ14811 for described uses).
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100.0%; Pred. No. 59;
Live 0; Mismatches
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2000US-0189974.
2000US-0199076.
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2000US - 0.217496
2000US - 0.220829
2000US - 0.220964
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2000US - 0.225266
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7; Conservative
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2000US-0229513.
2000US-0230437.
2000US-0230438.
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2000US-0231414.
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2000US-0235484.
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2000US-0236368.
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2000US-0246532.
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2000US-0231244.
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2000US-0239937
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2000US-0241785.
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2000US-0232397
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2000US-0249209
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01-SEP-2000;
01-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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02-0CT-2000;
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
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                                                                                 20000S-0249213.
20000S-0249214.
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2000US-0249217.
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2000US-0249245.
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20000S-0249297.
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Best Local Similarity 100°
Matches 7; Conservative
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
21-SEP-2000; 2
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and reatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK4942 to AAK84950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis \cdot
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llarity 100.0%; Pred. No. 78;
Consorvative 0; Mismatches 0; Indels
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05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0251990.
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100.0%; Pred. No. 80;
ive 0; Mismatches
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                                  9908-0156596.
9908-0157117.
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The invention relates to novel genes (ABAll004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the genes are. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital. (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischammias;
                                                                                                                                                                                                                                                                                                                                              (d) wound healing: (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human: prostate cancer antigen; cytostatic; uropathic; diagnostic; reproductive system; chromosomal marker; forensic; urinary disorder; chronic nephritis; blood-related disorder; thrombosis.
useful for preventing, diagnosing and/or treating nervous system
                                                           Claim 11; SEQ ID NO 5582; 1701pp + Sequence Listing; English
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Isolated polypeptide for treating, preventing and/or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e,g, diagnosis WPI; 2001-451929/48. N-PSDB; AAS40209.

Ruben SM:

Rosen CA, Barash SC,

Claim 11; SEQ ID No 361; 546pp; English.

polynucleotides (1) and polypeptides (11). (1) and (11) are useful for preventing, treating or ameliorating a medical condition when administered. (1), (11) and the antibody to (11) are useful for treating, preventing and or prognosing disorders related to the reproductive neptratisis, and blood-related disorders e.g. thrombosis. (11) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (11) and the anti-(11) antibody can be used in testing and detection in immunoassays. AAU22700-AAU32913 represent the human prostate cancer antigen amino acid sequences of the The invention relates to novel isolated human prostate cancer antigen

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Human: reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                           Gaps
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                                                                                                         Query Match 2.8%; Score 7; DB 22; Length 80; Best Local Similarity 100.0\%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number of human reproductive system related antigens. These can be use
in the prevention and treatment of reproductive system disorders,
including cancer. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #5839 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 4806; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acore () Fred, No. Te+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%; Score 7; DB 22; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 10.
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB38333 standard; Peptide; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                         17 NOV 2000; 2000US-0249300; 01-DEC-2000; 2000US-0250160; 01-DEC-2000; 2000US-0250191; 05-DEC-2000; 2000US-0251988; 05-DEC-2000; 2000US-0251988; 06-DEC-2000; 2000US-0251868; 08-DEC-2000; 2000US-0251868; 08-DEC-2000; 2000US-0251869; 08-DEC-2000; 2000US-0251989; 08-DEC-2000; 2000US-0251989; 08-DEC-2000; 2000US-0251989; 08-DEC-2000; 2000US-0251989; 08-DEC-2000; 2000US-0251989; 08-DEC-2000; 2000US-0251990; 05-JAN-2001; 2001US-0259678.
                                               2000US-0249216.
2000US-0249217.
2000US-0249218.
                                                                                    2000US-0249244.
2000US-0249245.
2000US-0249264.
                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                         2000US-0249214.
2000US-0249215.
                                                                                                                         2000US-0249265.
2000US-0249297.
                                                                                                                                                 2000US-0249299.
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                                                                                   17 - NOV - 2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB38333;
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Human brain expressed single exon probe encoded protein SEQ ID NO: 31052.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%; Pred. No. 1.1.
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                        26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GS-0024263.
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2000US-0207456.
2000US-0608409.
2000US-0532366.
2000US-0234687.
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30-JAN-2001; 2001WO-US00669
                                                               2000US-0180312
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17-0CT-2000
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                                                                                        Sednence
                                                                                                                             Query Match
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                                                                                                                                                                     probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #5811 encoded by probe for measuring placental gene expression.
                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                               The present invention provides a number of single exon nucleic acid
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                                                                                                                                      Example 4; SEQ 1D NO: 31052; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                     2.8%; Score 7; DB 22; Length 86; 00.0%; Pred. No. 1.1e+02;
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nes 0; Indels
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                                                                                                                                                                                                                                                                                                            100.0%; Pred. ....
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                                                 Chen W, Rank DR;
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                         (MOLE-) MOLECULAR DYNAMICS INC
04-OCT-2000; 2000GB-0024263.
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03-AUG-2000, 2000US-0632366.
21-SEP-2000, 2000US-0234687.
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2000US-0207456,
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Matches 7; Conservative
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                                                 Hanzel DK,
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                                                                          WPI; 2001-483446/52
                                                                                                                                                                                                                                                                  86 AA;
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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                      Gaps
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                                                                                                                 Length 86;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 6197.
                                                                                                                         100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
                                                                                                                 2.8%; Score 7; DB 22;
                                                                                                                                                                                                                                        AAG08597 standard; Protein; 92
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99US-0135353.
99US-0135629.
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99US-0132486.
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99US-0134941
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                                                                                                                                      Conservative
                                                         human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                                                86 AA;
                                                                                                                                                            14 LTGTSES 20
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990US-0147038 990US-0147038 990US-0147302 990US-0147303 990US-0147303 990US-01474016 990US-01474016 990US-0148341 990US-0148341 990US-0148341 990US-0148341 990US-0148341 990US-0149368 990US-0149368 990US-0149368 990US-0149368 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0150US 990US-0160US 990US-0160US 990US-0160US 990US-0160US 990US-0160US 990US-0160US 990US-0160US 990US-0160US 990US-0160US 990US-0160US	990S-0161359. 990S-0161360. 990S-0161361. 990S-0161920. 990S-0161992.
03 - Aug 11999 04 - Aug 11999 05 - Aug 11999 06 - Aug 11999 06 - Aug 11999 06 - Aug 11999 06 - Aug 11999 07 - Aug 11999 08 - Aug 11999 09 - Aug 11999 112 - Aug 11999 12 - Aug 11999 13 - Aug 11999 14 - OCT 11999 15 - Aug 11999 16 - Aug 11999 17 - Aug 11999 18 - Aug 11999 18 - Aug 11999 19 - Aug 11999 10 - Aug 11999 11 - Aug 11999 12 - Aug 11999 13 - Aug 11999 14 - OCT 11999 15 - OCT 11999 16 - OCT 11999 17 - OCT 11999 18 - OCT 11999 19 - OCT 11999 19 - OCT 11999 11 - OCT 11999 11 - OCT 11999 12 - OCT 11999 13 - OCT 11999 14 - OCT 11999 15 - OCT 11999 16 - OCT 11999 17 - OCT 11999 18 - OCT 11999 19 - OCT 11999 19 - OCT 11999 10 - OCT 11999 11 - OCT 11999 12 - OCT 11999 13 - OCT 11999 14 - OCT 11999 15 - OCT 11999 16 - OCT 11999 17 - OCT 11999 18 - OCT 11999 18 - OCT 11999 19 - OCT 11999 19 - OCT 11999 10 - OCT 11999 11 - OCT 11999 12 - OCT 11999 12 - OCT 11999 13 - OCT 11999 14 - OCT 11999 15 - OCT 11999 16 - OCT 11999 17 - OCT 11999 18 - OCT 11999	26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 28-0CT-1999; 28-0CT-1999;
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25. WAY  26. MAY  27. MAY  28. MAY  29. MAY  20.	7-JUL-1999; 3-JUL-1999; 2-AUG-1999; 2-AUG-1999; 2-AUG-1999;

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990S-01398999
990S-0140353.
990S-0140695.
990S-0140695.
990S-0140991.
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990S - 0142154
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99US-0139763.
99US-0139817.
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990S-0139119.
990S-0139452.
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99US-0147303.
99US-0147416.
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99US-0139460.
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99US-0147192.
                   10-10N-1999;
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19-10N-1999;
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16-JUL-1999;
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                                                                 Query Match 2.8%, Score 7; DB 21; Length 92; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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The present invention describes human secreted proteins encoded by polynucleotides obtained from adult testes, foetal brain, adult brain, bain (foetal and adult), foetal kidney, adult spleen, and adult thymus brain (foetal and adult), foetal kidney, adult spleen, and adult thymus con an interest that the polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, biological activities which would make them suitable for treating, broughsted activities include nutritional activity, cytokine and cell compressing activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, haematopoiesis regulating activity, clemokinetic activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Therapeutic compositions are also presently valuable for veterinary applications. AAZ52815 to AAZ52818 encode human secreted proteins, given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides and proteins having biological activities which make them suitable for treating, preventing or ameliorating medical conditions in humans or animals
                                                                                                                                                                                                                                                       Human, secreted protein; immunostimulatory; haemostatic, cytokine, proliferative; differentiative; chemotactic; chemokinetic; vaccine; thrombolytic; antlinflammatory; cytostatic; immunosuppressive;
                                                                                                                                                                                                                      Human secreted protein clone ys10_1 protein sequence SEQ ID NO:214.
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                                                                                                                  AAY73496 standard; Protein; 103 AA
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980.S-0103615.
980.S-011799.
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N-PSDB; AA252581.
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                                                            Gaps
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                                Query Match 2.8%; Score 7; DB 21; Lk Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                  AAG08595 standard; Protein; 110 AA
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99US-0123180.
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (1) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genefic disorders or other traits to assess biodiversity amino acid sequences of the invention.

The sequence adra for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.

The pub. The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
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                                                                                                                                                                                                            Novel human diagnostic protein #4827
                                                                                                                ABG04836 standard; Protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 100.
Matches 7; Conservative
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   26 GNDLSNV 32
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                                                                                                                                                                                                                                                                                            Homo sapiens.
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100.0%; Pred. No. 1.4e+02;
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99US-0149368.
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Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #12476.
                                                                                                                                                                        ABG12485 standard, Protein; 130 AA.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                         Novel human diagnostic protein #19843.
                                                                ABG19852 standard; Protein; 130 AA.
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23-AUG-2000; 2000US-0649167.
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RESULT 32
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                                                                                                                           Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
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                                                                                                                                                                                                                                                                                                                                                               diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
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                                                                                                                                                                                                                                                                                       Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID 4238; 71pp + CD-ROM; English.
                                                                                                     Human secreted protein, SEQ ID NO: 4238.
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                                        AAG00157 standard; Protein; 147 AA.
                                                                                                                                     gene therapy; chromosome mapping.
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(II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'Sa SA, Amshey S, Dahl CK, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL; Liu TE, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A; Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
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Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukacmia; acquired immune deficiency syndrome; AIDS; autoimmune disorder;
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2000US-0204226.
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                                                                              respiratory disorder.
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15-MAY-2000; 2
16-MAY-2000; 2
16-MAY-2000; 2
16-MAY-2000; 2
17-MAY-2000; 2
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17-MAY-2000;
17-MAY-2000;
                                                                                                                                    Homo sapiens.
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17-MAY-2000;
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24-FEB-2000;
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or supplementing the patient's own production of them. (1) and (11)

may be used to treat diseases, for example, cell proliferative disorder,

crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,

leukaemia, autoinmune disorders, and respiratory disorders. Additionally,

(1) may be used to produce the DITHFS, by inserting the nucleic acids

into a host cell and culturing the cell to express the protein. (1) and

its complementary sequences may also be used as DNA probes in diagnostic

samples, and therefore which patients may be in need of restorative

camples, and therefore which patients may be in need of restorative

therapy. (II) may also be used as antigens in the production of

antibodies and activity. The anti-DITHP antibodies and antagonists may

also be used to down regulate expression and activity. The anti-DITHP

antibodies may also be used as diagnostic agents for detecting the

presence of DITHPs in samples (e.g. by enzyme linked immunosorbant

assay (ELISA)). AAU19415-AAU19652 represent human diagnostic and

therapeutic (DITHP) polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic cardiant, antidiabetic, anoretic, hypotensive; hypertensive, antidarkinsonian; noctropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypotension; hypertension; myocardial infarction; atherosclerosis parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic;
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                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 7; DB 22; Length 162; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G protein-coupled receptor nGPCR-2459.
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08-MAR-2000; 2000US-0187715.

08-MAR-2000; 2000US-0187715.

08-MAR-2000; 2000US-0187828.

08-MAR-2000; 2000US-0187828.

08-MAR-2000; 2000US-0187829.
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                                                                                                                                                                                                                                                                                                                                                                  Seguence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 TQLQTL1 249
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The invention relates to novel isolated nucleic acid molecules encoding of protein coupled receptors termed nGPCR-x. nGPCR-x polynucleotides.

C polypeptides, and modulators may be used in the treatment of diseases and conditions such as infections, such as viral infections caused by HIV-1

(human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, anorexia, hypotension, hypertension, myocardial infarction.

C atherosclerosis), parkinson's disease, and psychotic and nervological disorders, including schizophrenia, migraine, major cheresion, anxiety, mental disorder, manic depression, and dyskinesias, such as Huntington's disease or Pourette's Syndrome and many other diseases and syndromes listed in the specification.

C nofPCR-x polynucleotides and polypeptides, as well as nGPCR-x modulators, may also be used in diagnostic assays for such diseases or content of the procession of the proces
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                                                                                                                                                                                                                                                                    Isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 31; Page 327; 336pp; English.
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                                (PHAA ) PHARMACIA & UPJOHN CO.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                           WPI; 2001-536778/59
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                                                                                                 Vogeli G, Wood LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA;
                                                                                                                                                                                                   N-PSDB; AAS30851
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30-AUG-2001.
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                                                                                                      capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                 genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY34584-Y25879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading
                        New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                             The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sinusitis, purulent otitis media; erythema nodosum: pharyngitis; vaccine; neutralising epitope.
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                                                                     Disclosure; SEQ ID NO 29325; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                             Query Match 2.8%; Score 7; DB 22; Length 187; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a Chlamydia pneumoniae protein.
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                                                                                                                                                                      sequences (ABL01840-
(ABB57737-ABB72072)
                                                                                                                                                                                                                                             Sequence 187 AA;
N-PSDB; ABL11614
                                                                                                                                                                                                                                                                                                                               152 LLTAVTI 158
                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET.
                                                interactions -
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Human, G-protein coupled receptor; GPCR; mental disorder; schizophrenia; attention deficit disorder; anxiety; depression; bipolar disorder; mentalous disorder; metabolic disorder; Huntington's disease; dementia; obesity; anorexia; metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis; type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer; cardiomyopathy; atheroscierosis; human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser; antidepressant; anorectic; gene therapy.
frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                       0; Caps
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                                                                                                                                                                                                                                                                 Length 194;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G Protein-Coupled Receptor (GPCR) polypeptide #19.
                                                                                                                                                                                                                                                              DB 20; Le
                                                                                                                                                                                                                                                                                                                    U; Mismatches
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                                                                                                                                                                                                                                                              2.8%; Score 7; [
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU25572 standard; Protein; 203 AA.
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2000US-0184305.
2000US-0184397.
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2000US-0217369.
2000US-0217370.
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                                                                                                                                                                               194 AA;
                                                                                                                                                                                                                                                                                                                                                                             242 KTQLQTL 248
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                                                                       polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, a GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as metabolic disorders such as obseity, anorexia and type 2 diabetes, cardiowascular disorders such as thromosis, myocardial infarction, cordiomyopathy and atherosclerosis, viral infections caused by HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAU29329-AAU29379 represent
                                    (GPCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to {\sf GPCR}
                 Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel mar regulated protein (NIMR) #33.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                          203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 LKISNSL 108
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The present invention describes cells originating in bone marrow or umbilical blood cells which are capable of differentiating into cardiomycotytes. Also described are: (1) cardiomycotytes produced by the differentiation of the cells; (2) a method for carrying out the differentiation into cardiomycotytes; (4) drug councinal and/or into cell types other than cardiomycotyes; (4) drug compositions into cell types other than cardiomycotyes; (4) drug compositions promoting the formation of heart muscle and regeneration of heart tissue which contain the cells; (5) a method for the production of antibodies which recognise the cells; (5) a method for screening factors which promote the proliferation of the cells; (7) a method for immortalising the treatment of heart disease which contain the immortalised cells; and (9) cell-free supernatant from the culture of the cells and its use in promoting their differentiation into cardiomycotytes. The cells are used in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction and in the study of cardiomycotyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cells capable of differentiating into cardiomyocytes and originating in
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Differentiation; heart muscle cell; cytokine; transcription factor; proliferation; surface antigen; heart disease; cardiomyocyte; bone marrow; umbilical blood cell; heart muscle degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease
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Escherichia coli NIMR amino acid sequences of the invention
                                                                                           Length 211;
                                                                                                                            0; Indels
                                                                                         DB 22; Le
                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          Rat dHAND protein sequence SEQ ID NO:21.
                                                                                         2.8%; Score 7; I
100.0%; Pred. No.
ative 0; Mismatch
                                                                                                                                                                                                                                                                                             AAB99925 standard; Protein; 217 AA.
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                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001 (first entry)
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myocardial infarction.
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                                                                                                           Best Local Similarity
Matches 7; Conserv
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WO200148151-A1.
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                                                                       Homo sapiens
                                                                                                              05-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New adult bone marrow-originated cells capable of differentiating into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heart muscle cells, applicable as remedies for various heart diseases
particularly with damaged heart muscle accompanying degeneration
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                   Angiogenesis; cardiant; cell differentiating agent; bone marrow; heart muscle cell; heart disease; rat; dHAND.
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sequences used in the exemplification of the present invention.
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5. 2.5e+02;
cches 0; Indels
                                                Query Match 2.8%; Score 7; DB 22; Length 217; Best Local Similarity 100.08; Pred. No. 2.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.5
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                   AAG64324 standard; Protein; 217 AA.
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                                                                                                                                                                                                                                Rat dHAND protein.
                                                                                                                                                                                                                                                                                  Rattus norvegicus.
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The present invention provides cells originating in the human bone marrow or umbilical blood cells which are capable of differentiating into cardiomycoytes. These cells are useful in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction, and the study of cardiomycoyte differentiation. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cells capable of differentiating into cardiomyocytes and originating in bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease
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Heart muscle cell differentiation related protein SEQ ID NO: 21.
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                                                               Heart muscle cell; human; cell differentiation; heart disease.
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100.0%; Pred. No. 2.5
Live 0; Mismatches
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    scapularis Salp25A protein sequence.

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02-NOV-2000; 2000WO-JP07741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WP1; 2001-425656/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ixodes scapularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH48230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 LKSTVSS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 lkstvss 195
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Sedirence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                   Region
                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY13944
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    This sequence is an ixodes scapularis polypeptide of the invention.

The proteins of the invention are 15 tick Salp proteins. The proteins. The proteins antibodies against them or planmaceutical composition comprising a fusion protein or a multimeric protein and at least one additional non-ixodes capularis polypeptide, can be administered to a subject to confer tick immunity and therefore prevent infection by a tick-borne disease. Inhibiting acceptation factor Xa activity comprises administering to a subject a polypeptide selected from Salp14A, Salp9A or a fragment of these having Xa inhibiting activity, inhibiting histamine activity comprises administering a cativity, inhibiting histamine binding fragment to a subject, and inhibiting or preventing an inflammatory response comprises administering a polypeptide selected from a Salp15, and protein or its immunogenic fragment may be used to produce monoclonal antibodies that are screened for their ability to confer tick immunity when used to immunise naive animes. The autibody can be used to screen for expression of I. scapularis polypeptides, either in the profice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other samples in which proteins may be present, and for purifying or removing polypeptides from a given sample to block or bind to specific epitopes on the polypeptides and to direct various molecules, such as
                                                                                                                                                     Novel ixodes scapularis polypeptides for conferring tick immunity and for preventing the transmission of tick-borne pathogens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human transforming growth factor; TGF; TGF-alpha-HIII; anglogenesis; embryogenesis; ocular disorder; kidney disorder; liver disorder; neuronal disorder; alopecia; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 7; DB 22; Length 222; 100.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human transforming growth factor alpha HIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= signal_peptide
/note= "putative"
26..229
/label= mature_protein
1..177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW27087 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                               Claim 20; Fig 16; 137pp; English.
                                                                            Das S;
03-DEC-1999; 99US-0169048.
16-OCT-2000; 2000US-0240716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                            Kantor FS, Fikrig E,
                                                                                                         WPI: 2001-367810/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AA;
                                               (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxins, to ticks.
                                                                                                                        N-PSDB; AAA91501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 VLLCGVL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 v]]Cqv[ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW27087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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growth factor (TGF) alpha malaged. TGF-alpha HIII. The protein can stimulate angiogenesis, embryogenesis, cell differentiation and function. It can be used for therapeutic purposes for restoration or enhancement of neurological functions diminished as a result of trauma or other damaging pathologies such as AIDS dementia and senile dementia, to treat coular disorders, e.g. corneal inflammation, to destroy target cells, to treat tumours, kidney or liver disorders or to treat wounds, burns or ulcers. The polypeptide can also be used in the modulation of angiogenesis, bone resorption, immune response, and synaptic and neuronal effector functions, or the arachidonic acid cascade. It can also be used in apperproliferative disorders such as inflammation or psoriasis and for alopecia, hair loss or other skin conditions which affect hair follicular development. Anragonists to TGF-alpha-HIII can be used for treating tumours or skin disorders such as sporiasis. The products can also tumours or skin disorders such as sporiasis. The products can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane protein; human; cell membrane; proliferation; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This protein has been putatively identified as a human transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human transforming growth factor-alpha homologue - used for developing products for treating e.g. neurological disorders, kidn and liver disorders, tumours, wounds, hair loss or skin disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell differentiation; carcinostatic agent; probe; gene therapy; signal transduction; apoptosis; inhibitor; phopshatidylethanolamine N-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 7; DB 18; Length 229; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels.
/label- soluble_portion_of_protein
126..177
                                                                                                              178..204
/label= transmembrane_portion
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                                                                         /label- active_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 47; 63pp; English.
                                                                                                                                                                                        /note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US00149.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-372817/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT85082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-1996;
                                                                                                                                                                                                                                                                       WO9725349-A1
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AAB33419;
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO246; EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
                                                                                                                                                                                                                                   All of the proceins exist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may be useful as carcinostatic agents or as antipagns for preparing antibodies against the proteins. The CDNAs can be used as probes for gene diagnosis and gene sources for gene therapy, as well as for large-scale expression of the proteins. The HPO149B (see AAY1333) protein may be associated with apoptosis, and therefore useful in inhibition of apoptosis. The HPO1962 (see AAY13943) protein can be used to treat diseases associated with
                                                                                                                                                                                                                                                                                                                            phopshatidylethanolamine N-methyltransferase. The proteins are identified by the presence of a hydrophobic transmembrane region, knowledge of the protein function is not required, as in e.g. methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                           This sequence is a human transmembrane protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 7; DB 20; Length 229; 100.0%; Pred. No. 2.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                   Human transmembrane proteins and nucleotide sequences
                                                                                                                                 Kato S, Kobayashi M, Sekine S, Yamaguchi T;
                                                                                                                                                                                                        Claim 1; Page 90-91; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY05282 standard; Protein; 229 AA.
                                                                                                         (SAGA ) SAGAMI CHEM RES CENT.
                                                                                97JP-0276271.
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97US-0059114.
                                                            98WO-JP04475
                                                                                                                                                                N-PSDB; AAX36812, AAX36813.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
                                                                                                     (PROT-) PROTECENE INC.
                                                                                                                                                      WPI; 1999-277268/23
                                                                                                                                                                                                                                                                                                                                                             expression cloning.
                                                                                                                                                                                                                                                                                                                                                                                 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 TQLQTLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 tqlqtli 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGF-8 homologue.
                                                                                08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1997;
17-SEP-1997;
                                                            05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9914327-A2
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                   WO9918203-A2
                                        15-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY05282;
                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY05282
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This sequence represents the EGF-like homologue PRO240.

The invention relates to autibodies (Ab) that bind to any of the prolypeptides (1) designated PRO187; PRO533; PRO2149; PRO240; PRO211; PRO240; PRO216; PRO246 or EBAF-2. The Ab, or other agents that inhibit expression and/or activity of (1) are used: (1) to inhibit growth of tumours; and (il) as diagnostic/prognostic reagents for detection or quantification of (1) in cells or tissues, by standard immunoassays, with overexpression being indicative of cancer. For therapeutic use, the Ab may be conjugated to a toxin, chemotherapeutic agent or radioisotope. Genes expressing (1), many of which are growth factor homologues, are overexpressed in some cases of cancer.
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M dermatological; antiarthritic; antirheumatic; immunosuppressive;

M antianaemic; hepatotropic; autidiabetic; nootropic; neuroprotective;

antianaemic; hepatotropic; virucide; antibsoriatic; antiallergic;

M antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

M steoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

M idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

M systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

M autoimmune thrombocytopaenia; immune-mediated renal disease;

M inflammatory bowel disease; gluten-sensitive enteropathy;

autoimmune disease; immune-mediated skin disease;

M inflammatory bowel disease; gluten-sensitive enteropathy;

M autoimmune disease; immune-mediated skin disease;

M mmunological disease; transplantation associated disease;

M graft rejection; graft-versus-host-disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against specific proteins overexpressed in tumours
                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A, Gurney A, Hillan K, Lawrence DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.8%; Score 7; DB 20; Le Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 7; Conservative 0; Mismatches 0;
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                                                                        97US-0062125.
97US-0062285.
97US-0062287.
                                                                                                                                                                                               97US-0062816.
97US-0063704.
97US-0059117
97US-0059263
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                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-229532/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB: AAX28432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 TOLQTLI 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200053758-A2
                                                                        15-0CT-1997)
17-0CT-1997)
17-0CT-1997)
24-0CT-1997)
29-0CT-1997)
                                                                                                                                                                                                                                                                                                                                                                                                      Botstein D,
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic infammatory myopathies, Sjogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic annaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune-mediated skin diseases, allergic diseases, immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney AL, Hebert C, Henzel W; D, Shelton DL, Smith V; Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ, Baker KP, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 33; Fig 12; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan J,
                                                                                                                                                                                                                                                                                                                                                                             99WO-US28301.
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99US-0162506
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990S-0134287
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                        02-MAR-2000; 2000WO-US05841
                                                                                                      99US-0128849
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Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000;
06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
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30-DEC-1999;
                                                                                                                      20-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stewart TA,
                                                                                                                                            04-MAY-19
14-MAY-19
02-JUN-1
                                                                                                                                                                                                                                                                                             15-SEP-19
05-OCT-19
29-OCT-19
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This sequence represents a human PRO240 amino acid sequence. PRO240

Shares Sequence homology with the D. melanogaster serrate precursor

protein and the Gallus gallus C-serrate-1 protein. The PRO240 gene is

located on chromosome 2. The invention relates to isolated antibodies

which bind to a polypeptide. The "PRO" polypeptides are encoded by genes

which are over expressed in the genome of tumour cells. Vectors and host

cells comprising the nucleic acid encoding the antibodies are used in the

production of the antibodies. The antibodies and nucleic acids encoding

them are used for diagnosing a tumour na mammal. The antibodies are

used for inhibiting the growth of tumour cells and identifying compounds

that inhibit a biological or immunological activity of and/or expression

of a PRO187, PRO533, PRO214, PRO240, PRO211, PRO240, PRO211, PRO246 or

RR0317 polypeptide. The antibody can be used in antibody dependent enzyme

mediated prodrug therapy (ADEPT) by conjugating the antibody to a

mediated prodrug the argyme which converts a prodrug to an anti-cancer

drug. The antibodies can be fluorescently labelled and monitored by light

microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAR33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human; cell growth proliferation; serrate precursor; C-serrate-1; ADEPT; antibody dependent enzyme mediated prodrug therapy; chromosome 2.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated antibodies which bind to specific polypeptides used for diagnosis and treatment of neoplastic cell growth and proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                       DB 21; Length 229;
5. 2.6e+02;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                100.0%; Pred. No. -
                                                                                                                                                                                         2.8%; Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY88570 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO240 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 8; 200pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                               7; Conservative
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                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                         229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA30036.
                                                                                                                                                                                                                                                                         243 TOLOTLI 249
                                                                                                                                                                                                                                                                                                              117 tqlqtli 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000.
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                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                            RESULT 48
                                                                                                                                                                                                                                 Matches
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                                                                                                                                                                                                                                                    q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents the amino acid sequence of human transforming growth factor (TGF) alpha HIII. TGF alpha HIII nucleic acid and protein may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression, for example immune
                                                                                                                                                                                                                                                                                                                                                                                 diagnostic; therapeutic; immune disorder; multiple sclerosis; systemic lupus erythematosus; human immuno-deficiency virus; HTV; hyperproliferative disorder: Gaucher's disease; cardiovascular disease; Scimitar syndrome; Chaqa's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder: corneal graft; neovascularisation; wound healing; diabetic retinopathy; neurological disorder; coronary arteriosclerosis; Alzheimer's disease, Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding human transforming growth factor alpha III (76\mathrm{Fa}), useful for preventing, diagnosing and/or treating e.g. Cancer
                                                                                                                                                                                                                                                                                                                                                                   Human; TGF alpha Hill; transforming growth factor alpha Hill; cancer;
                                                                                                           Gaps
                                                                                                        .;
                                                                            Length 229;
                                                                                                        0; Indels
                                                                           DB 21; L¢. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mature TGF alpha HIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Transmembrane region"
                                                                                                                                                                                                                                                                                                                                      Transforming growth factor (TGF) alpha HIII.
                                                                         2.8%; Score 7; DB 2
100.0%; Pred. No. 2.6
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                              AAU04295 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Fig 1; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Parkinson's disease -
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126..177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26..229
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N-PSDB; AASO8543.
                                                                            Query Match
Best Local Similarity
                               229 AA;
                                                                                                                                     243 TOLOTLI 249
                                                                                                                                                                   117 tqlqtli 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1999;
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                                                                                                                                                                                                                                                                           AAU04295;
                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                  49
                                                                                                          Matches
                                                                                                                                                                                                                                 AAU04295
                                                                                                                                                                                                                  RESULT
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arteriosclerosis), anglogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis (full details given in specification). Additionally, the nucleic acid may be used to produce the secreted polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. It may also be used as a DNA probe in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients may be in need of restorative therapy. The polypeptides may also be used as antigens in the production of antibodies against Trg alpha HIII antibodies may also be used as diagnostic agents for detecting the presence of TGF alpha HIII antibodies may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO240; UNQ214; human; immune disease; autoimmune disease; antitheumatic; antiarthritic; antiinflammatcry; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallergic; immunostimulant; serrate; lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "epidermal growth factor domain cysteine
                                                                                                                                                                                                                                                                                                                                                                                                    in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
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0
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Mn. 2.6e+02;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note~ "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 7; DB 2
100.0%; Pred. No. 2.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pattern signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB20112 standard; Protein; 229 AA.
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/note= "A>
172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7: Conservative
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181..193
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/note= "N
132..138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 AA;
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/note= "N-myristoylation site"
177..183
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                                                                                                                                       15-MAR-2000; 2000WO-US06884.
                                                                                                                                                                99US-0144758.
                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                   2001-103149/11.
                                                                                                                                                                                                                                                                               N-PSDB; AAF30054
                                                                                     WO200105972-AI.
                                                                                                                                                                                                                   Ashkenazi AJ,
                                                                                                                                                                20-JUL-1999;
                                                                                                              25-JAN-2001.
                                                                                                                                                                                                                                           Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
lan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating an immune response in a mammal using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
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2.8%; Score 7; DB 22; Length 229; 100.0%; Pred. No. 2.6e+02;

Best Local Similarity

Query Match

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Gaps
·.
0; Indels
0; Mismatches
                                                                                                         6, 2002, 16:46:46
7; Conservative
                                                                                                       Search completed: August
Job time: 333 sec
                          243 TQLQTL1 249
                                                   117 tqlqtli 123
 Matches
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APPLICANT: Tomasz, Alexander
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Ave, Continental Plaza, 4th CITY: Hackensack Ave, Continental Plaza, 4th CITY: Hackensack STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08679635A Patent No. 5985643
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                   (without alignments) 464.627 Million cell updates/sec
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1 MLQLWKLVLLCGVLTGTSES......NVIQQVVDNPQHKTQLQTLI 249
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                                                                                                                             August 6, 2002, 16:39:58; Search time 13.09 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-550-338-2
US-09-295-186-17
US-08-483-101-4
US-08-250-789A-26
US-08-250-789A-26
US-08-350-789A-26
US-08-300-928C-23
US-08-430-944D-23
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US-08-431-184-22
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US-08-431-184-22
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US-08-430-944D-78
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                                                                                                                                                                                                                                                                                                                                                                         231628 seqs, 24425594 residues
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                                                                                      - protein search, using sw model
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                   Word size
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                                                                                                                                Run on:
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Patent No. 5
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                                                                                                                Seguence
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US-08-430-014-78
US-08-431-184-78
PCT-0839-72-14
US-08-383-75-2-14
US-08-383-75-7
US-08-58-72-7
US-08-58-72-7
US-08-58-72-7
US-08-58-72-7
US-08-58-72-7
US-08-58-72-7
US-08-68-72-7
US-08-68-72-7
US-08-68-72-7
US-08-68-72-7
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US-08-68-72-7
US-08-93-08-11
US-08-93-09-11
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: USUDA, YOSHIHITO
APPLICANT: USUDA, YOSHIHITO
APPLICANT: MIRARA, YOSHIHITO
APPLICANT: MIRARA, YOSHIHITO
APPLICANT: MIRARASHI OSAMU
TITLE OF INVENTION: GMP Synthetase and Gene Coding for the Same
TITLE OF INVENTION: GMP Synthetase and Gene Coding for the Same
CURRENT APPLICATION UNIMER: US/09/550,338
CURRENT APPLICATION NIMBER: US/09/04-14
PRIOR FILING DATE: 1949-04-12
NUMBER OF SEQ ID NATE: 1949-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.2%; Score 8; DB 2; Length 561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,635A
FILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 21;
tive 0; Mismatches
                                                                                       IMBER: US/08/679,635A
10-JUL-1996
                                                                                                                                                                                      NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-141
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Patent No. 6127137
PEBERAL INFORMATION:
APPLICANT: Hasida, Miyoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09550338
Patent No. 6210951
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin version 3.0
                                                                                                                                                                                                                                                                             TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAWASAKI, Hisashi
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-679-635A-7
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APPLICANT: KAWASAKI
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APPLICANT: Stringer, Mary Ann
TITLE OF INVENTION: An Acidic Phospholipase, Production, and
TITLE OF INVENTION: Achoes of Using Thereof (As Amanded)
FITLE OF INVENTION: Methods of Using Thereof (As Amanded)
FILE REFERENCE: 4953.204-US
CURRENT APPLICATION NUMBER: US/09/295,186B
CURRENT APPLICATION NUMBER: 1215/96
PRIOR FILING DATE: 1995-10-31
PRIOR FILING DATE: 1995-10-31
PRIOR FILING DATE: 1997-10-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF TITLE OF INVENTION: ISOLATING SAME NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%; Score 7; DB 3; Length 664; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,396A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-333BX
TELECOMMUNICATION INFORMATION:
TELEFANE: (617) 842-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,488
Tsutsumi, No. 61271371ko
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Saccharomyces cerevisiae US-09-295-186-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08477396A
Patent No. 5872235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: .MEDIUM TYPE: Floppy disk
                           Halkier, Torben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Lan Bo
APPLICANT: Bao, Shideng
APPLICANT: Liu, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 GLNLSFP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GLNLSFP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boston
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 17
LENGTH: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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APPLICANT: COLE, PALLID
APPLICANT: COLE, PALLID
APPLICANT: KULIYAN, JOHN
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION UNMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER PLING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PALENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%; Score 7; DB 3; Length 1048; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Peptides That Bind to IL-2 Receptors NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,789A
FILING DATE: 27-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 563597viel, Vernon A.
RECISTRATION NUMBER: 32.483
REFERENCE/COCKET NUMBER: 16528A-57/1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 26, Application US/08250789A
; Patent No. 5635597
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: 14M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Saccharomyces cerevisiae US-09-356-952-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barrett, Ronald W. APPLICANT: Chernov-Rogan, Tania APPLICANT: Davis, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  APPLICANT: Boriack-Sjodin, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 amino acids
                          APPLICANT: Margarit, S. M. APPLICANT: Bor-Sogi, Dafna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 SLDLLTA 155
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                                                                                                                                                                                                                                                                                                                                            LENGTH: 1048
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
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                                                                                                                                                                             Query Match 2.8%; Score 7; DB 2; Length 777; Besi Local Similarity 100.0%; Pred. No. 2.3e+05; Matches 7; Conservative 0; Mismatches 0; Indels Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%; Score 7; DB 2; Length 866; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Caron, Judy
TITLE OF INVENTION: CS2 Proteins and Coding Sequences
CORRESPONDENCE. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRYMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/483,101
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferber, Donna M.
REGISTRATION UNBHER: 33878
REFERENCE/DOCKET NUMBER: 6-95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09356952; Patent No. 6117663; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08483101
Patent No. 5932715
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Scott, June R. APPLICANT: Froehlich, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acids
                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                             TYPE: amino acid
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Colorado
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                                                                                                             US-08-477-396A-4
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                                                                                                                                                                          Query Match
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ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
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COMPUTER READABLE FORM:
MEDLIW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 23, Application US/08430944D
; Patent No. 6025162
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103
                                                                                                                                                                 SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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3Y: linear
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STREET: 20
      WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 LSLLDK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                            COUNTRY:
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                                            Gaps
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TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
                                                                                                                                                                                                                                                                                     APPLICANT: Barrett, Ronald W.
APPLICANT: Chernov-Rogan, Tania
NUMBER OF SEQUENCES: 194
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.4%; Score 6; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 45; Matches 6; Conservative 0; Mismatches 0; Indels
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DB 1; Length 12; 45;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,789A
FILLING DATE: 27-MAY-1994
Query Match 2.4%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           Sequence 62, Application US/08250789A Patent No. 5635597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Maicolm L. et a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: poptide
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: ONe Mainer
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                  168 VAVLGE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 VAVLGE 173
                                                                                                          RESULT 8
US-08-250-789A-62
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4%; Score 6; DB 3; Length 14; 100.0%; Pred. No. 52; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28 Apr.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-Apr.1995
PRIOR APPLICATION NUMBER: US 08/300,928
FILING DATE: US 08/300,928
FILING DATE: US-SEPT-1994
                                                                                                                                                                                                                                                                                   002.6US(IMI-044)
APPLICATION NUMBER: US/08/300,928C FILING DATE: September 2, 1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/807,529 FILING DATE: December 13, 1991 CLASSIFICATION: 435
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Gaps
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TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN

TITLE OF INVENTION:
                      0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.4%; Score 6; DB 3
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches
100.0%; Pred. No. 52;
                    0; Mismatches
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 103
CORRESSENDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 13, Application PC/TUS9302462
; GENERAL INFORMATION:
                                                                                                                                                                                           Sequence 23, Application US/08431184
Patent No. 6120769
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REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gefter, Malcolm L.
Garman, Richard D.
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Briner, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617)227-7400
(617)742-4214
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                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
FRACMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Best Local Similarity
Matches 6; Conservat
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                        183 LSLLDK 188
                                                                                                                                                                                                                                                                                                                                                                                    Boston
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                                                                                             3 LSLLDK 8
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PCT-US93-02462-13
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APPLICANT:
APPLICANT:
                                                                                                                                                      RESULT 12
US-08-431-184-23
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APPLICANT:
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CITY: B
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APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                         DB 3; Length 14;
5. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
RECISTRATION NUMBER: 36, 207
REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         Query Match 2.4%; Score 6; DB 3 Best Local Similarity 100.0%; Pred. No. 52; Matches 6; Conservative 0; Mismatches
                NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/430,014 FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08430014 Patent No. 6048962
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TELEFAX: (617) 227-7400
INPORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                           amino acid
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2.4%; Score 6; DB 3; Length 14;

Query Match

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REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)272-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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28-APR-1995
  APPLICATION NUMBER: US/U8/300,928C
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FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                        September 2, 1994
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
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REGISTRATION NUMBER: 36,20
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                                                                                                                                                                                                                                                                                                                                          16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-APR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                  linear
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APPLICANT: Bruce I
                        FILING DATE: Se
CLASSIFICATION:
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Patent No. 6019972.
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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APPLICANT: MOTVILLE, MALCOLM
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
UMMER OF SEQUENCES: 14
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: IMMULOGIC PHARMACEUTICAL CORPORATION 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPC-031PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/884,718 FILING DATE: 15-RAY-1992 APPLICATION NUMBER: 07/857,311 FILING DATE: 25-WAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: US 07/884,718
APPLICATION NUMBER: US 07/857,311
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASC11 TEXT
CURRENT APPLICATION DATA:
                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mandragouras, Amy E. RATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 227-7400 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 amino acids
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                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                         USA
02109
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                                                                                                                            Boston
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3 LSLLOK 8
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                                                                                                                                                                      COUNTRY:
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                                                                                                                                           STATE:
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APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.4%; Score 6; DB 3; Length 16; Best Local Similarity 100.0%; Pred. No. 58; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
REFERENCE/TOCKET NUMBER 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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Sequence 22, Application US/08431184 Patent No. 6120769 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : (617)227-7400
(617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.08
Matches 6; Conservative
                                                                                                        NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-431-184-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                  Massachusetts
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                      02109
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                                                                                                                                                                                                  STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                             Patent No. boxxxx.
GENDARL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 6; DB 3; Length 16; 100.0%; Pred. No. 58; tive 0; Mismatches 0; Indels
                                                                                                                          DB 3; Length 16;
. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: IMMULOGIC PHARMACEUTICAL CORPORATION 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       002.6US(IMI-044)
                                                                                                                        2.4%; Score 6; DB 3
100.0%; Pred. No. 58;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08430014
Patent No. 6048962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 002.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,20
                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 16 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-430-014-22
                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
   TYPE: amino acid
                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALTHAM
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                                                                                                                                                                                                                                                                                                           US-08-430-014-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-431-184-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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APPLICANT: Bruce L. ROGERS et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 16; . 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gefter, Malcolm L.
APPLICANT: Gerenate, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Kuo, Mei-chang J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
OUNBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 6; DB 3
100.0%; Pred. No. 58;
tive 0; Mismatches
                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US93-02462-12; Sequence 12, Application PC/TUS9302462; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1M,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
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APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.4%; Score 6; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 68; Matches 6; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: IMMULOGIC PHARMACFUTICAL CORPORATION STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             002.6US(IMI-044)
                                                                                                                               IPC-027/imi-015
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CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 20, Application US/08300928C
; Patent No. 6019972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                NAME: Channing, Stacey L.
REGISTATION UNDRER: 31,095
REFERENCE/DOCKET UNDRER: IPC-CECOMMUNICATION INFORMATION:
TELEPHONE: (GIT) 494-0060
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      December 13, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEC ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                      19 amino acids
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-07-807-529A-10
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                                                                                                                                                                                                                                                        AMINO ACID
                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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2.4%; Score 6; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morvile, Malcolm
APPLICANT: MORVINE: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAMULOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                IPC-031PC
                                                                                                                      APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/07807529A
Patent No. 5547669
GENERAL INFORMATION:
APPLICANT: Royers, Bruce L.
APPLICANT: Mordenstern
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIL TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morgenstern, Jay
Bond, Julian F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal
COMPUTER READABLE FORM:
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TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One
                                                                                                                                          FILING DATE: 1 CLASSIFICATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Patent No. 6048962
GENERAL INPORTION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
                                                                                                                                                                                                                                                                                                                           A HUMAN T CELL REACTIVE FELINE PROTEIN
                                             0; Indels
2.4%; Score 6; DB 3; Length 19; 100.0%; Pred. No. 68; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.4%; Score 6; DB 3;
100.0%; Pred. No. 68;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REPERDELPOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/430,014 FILING DATE: 27-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/300,928 FILING DATE: 02-SERT-1994 APTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               Sequence 20, Application US/08430944b
Patent No. 6025162
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    APPLICANT: Bruce L. Rogers et al. TITLE OF INVENTION: A HUMAN T CEI TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
    Query Match 2.4%
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)742-4214
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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; FRAGMENT TYPE: internal
US-08-430-944D-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                                      183 LSLLDK 188
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APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULGGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    002.6US(IMI-044)
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100.0%; Pred. No. 68;
tive 0; Mismatches
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STREET: 28 State Street
                                                                                                                                                                                                                                           SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR TOTAL NIMBER: 08/300,928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                Massachusetts
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                                                                             STATE: MALTHAM
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CLASSIFICATION:
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-mv: Boston
                                                                                                                                    USA
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                                                                                                                                  COUNTRY:
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2.4%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOAG, JOLIAN F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morvile, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     Query Match 2.4%; Score 6; DB 5; Best Local Similarity 100.0%; Pred. No. 68; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NIMBER: US/07/807,529A
FILING DATE: 1991]213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Sequence 29, Application US/07807529A ; Patent No. 5547669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 1PT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rogers, Bruce L. APPLICANT: Morgenstern, Jay APPLICANT: Bond, Julian F.
                                     LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 20 amino acids
AMINO ACID
         SEQUENCE CHARACTERISTICS:
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                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US93-02462-10
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; FRAGMENT TYPE: internal
US-07-807-529A-29
                                                      AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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GENERAL INFORMATION:
APPLICANT: Garman, Richard D.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: From Stein, Julia L.
APPLICANT: Briner, Thomas J.
APPLICANT: APPLICANT: ABICOLM
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 14
CORRESPONDENCE ADDRESSE: ABILIVE & COCKFIELL)
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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2.4%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred, No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ 1D NO: 20:
SEQUENCE CHARACTER STICS:
LENGTH: 19 aming acids
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REGISTRATION NUMBER: 36,207
PEFERENCE/DOCKET NUMBER: JPC-031PC
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
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APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/884,718 FILING DATE: 15-MAY-1992 APPLICATION NUMBER: 07/857,311 FILING DATE: 25-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                     inear
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STREEFF: bu ...
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PCT-US93-02462-10
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
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                                                                                                                                                       Patent No. 601557.
GENERAL INFORMATION:
APPLICANT GEFER MALCOLM L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78. Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: BRUCE L. ROGETS et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
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                                                                                                                                                                                                            TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL, REACTITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIORADILICATION DATA:
PRIORADILICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEYAGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REPERENCE/DOCKET NUMBER: 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
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100.0%; Pred. No. 71;
tive 0; Mismatches
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FILING DATE: September 2, 1994
                                                                                                              US-08:300-928C-78
; Sequence 78, Application US/08300928C
; Patent No. 6019972
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: SeCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 LSLLDK 188
183 LSLLDK 188
                                    1 LSLLDK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Gaps
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TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULGGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                      SOFTWAKE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.4%; Score 6; DB 3;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/300,928
FILLNG DATE: 02-SEPT-1994
ATTONNEY AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36_207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/430,944D FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/430,014 FILING DATE: 27-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Sequence 78, Application US/08430014 ; Patent No. 6048962
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APPLICATION NUMBER: 08/300,928
                                                                     COMPUTER READAHJE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WALTHAM
Massachusetts
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0; Gaps

COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC computeR: LBM PC compatible
COMPUTER: LBM PC computeR: LBM PC computeR: LBM

2.4%; Score 6; DB 3; Length 20;

US-08-431-184-78

Query Match

ö ô Gaps ; ö 0; Indels 0; Indels Length 20; APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Matcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION 2.4%; Score 6; DB 5; 100.0%; Pred. No. 71; tive 0; Mismatches 100.0%; Pred. No. 71; tive 0; Mismatches COLLING DATE: 1990...
FILING DATE: 1990...
FLING PRICATION:
PRIOR APPLICATION NUMBER: US 08/006,116
APPLICATION NUMBER: US 08/006,116
APPLICATION NUMBER: US 08/006,116
APPLICATION NUMBER: US 08/006,116
APPLICATION NUMBER: US 07/684,718 SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/02462 FILING DATE: 19930328 Sequence 14, Application PC/TUS9302462 GENERAL INFORMATION: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: 07/857,311 FILING DATE: 25-MAR-1992 ATTORNEY/AGENT INFORMATION: E: LAHIVE & COCKFIELD 60 State Street US-08-383-753-7 Sequence 7, Application US/08383753 ; Patent No. 572384 ; GENERAL INFORMATION: REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 14: APPLICANT: Gefter, Malcolm L. APPLICANT: Garman, Richard D. APPLICANT: Greenstein, Julia 1 Mandragouras, Amy E. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk Best Local Similarity 100.0 Matches 6; Conservative Best Local Similarity 100.0 Matches 6; Conservative SEQUENCE CHARACTERISTICS: 20 amino acids MOLECULE TYPE: peptide FRAGMENT TYPE: internal NUMBER OF SEQUENCES: I CORRESPONDENCE ADDRESS: FILING DATE: 15-JAN-APPLICATION NUMBER: FILING DATE: 15-MAY-APPLICATION NUMBER: AMINO ACID linear Boston USA 183 LSLLDK 188 183 LSLLDK 188 COUNTRY: US ZIP: 02109 ΜA ADDRESSEE: PCT-US93-02462-14 PCT-US93-02462-14 TOPOLOGY: LENGT'H: STREET: STATE: Query Match NAME: RESULT 31 ó qq

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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 1HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUMENT APPLICATION DATA:
APPLICATION NUMBER: US/U8/959,512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schatz, Peter J.
TITLE OF INVENTION: Biotinylation of Proteins
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,753
FILING DATE: 03-FEB-1995
APPLICATION NUMBER: US 08/099,991
FILING DATE: 30-00L-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
           APPLICATION NUMBER: US 08/099,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/08959512
; Patent No. 5932433
                                                                                                             REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
                                                                                             30,223
                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                 FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                       NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                              22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 22 amino acids
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CITY: San Francisco
CTATE: California
                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-586-772-7
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; MOLECULE TYPE: peptide
US-08-959-512-7
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                          LENGTH: 22 amino
TYPE: amino acid
STRANDEDNESS: sin
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2 QPVAVL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94105
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                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: Patentin Release #1.0, Version #1.25
SURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,753
FILING DATE: 03-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/099,991
FILING DATE: 30-JUL-1993
ATMONEY/AGENT INPORMATION:
APPLICANT: Schatz, Peter J.
TTLE OF INVENTION: Bictinylation of Proteins
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schatz, Peter J.
TITLE OF INVENTION: Biotinylation of Proteins
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No. 77;
tive 0; Mismatches
                                                                                                             One Market Plaza, Steuart Tower
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APPLICATION NUMBER: US/08/586,772
FILING DATE: 03-FEB-1995
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1038.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-586-772-7
; Sequence 7, Application US/08586772
; Patent No. 5874239
                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS AME
SOPTHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hest Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: peptide US-08-383-753-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: ONE MAINCE
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                               San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 QPVAVL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QPVAVL 7
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                                                                                                                                                                           COUNTRY:
                                                                                                             STREET:
CITY: S
                                                                                                                                                       STATE:
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ADDRESSEE: Sheridan muss
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100603.8
FILING DATE: 17-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08807332B
Patent No. 5959074
                                                                        340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                         Lewis J
BER: 38,522
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: RA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (973) 235-4387
TELEFAX: (973) 235-2363
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                             Nutley
New Jersey
                                                                                                                U.S.A.
07110
R Pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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STREET: 1/v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 VAVLGE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 VAVLGE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                           STREET:
                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                        Gaps
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                                    0; Indels
2.4%; Score 6; DB 2; Length 22; 100.0%; Pred. No. 77; Uve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.4%; Score 6; DB 4; Length 22; Best Local Similarity 100.0%; Pred. No. 77; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anownsend Khourie and Crew STREET: One Market Plaza, Steuart Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                   APPLICANT: Schatz, Peter J.
TITLE OF INVENTION: Biotinylation of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIASTFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/383,753
FILING DATE: 03-FEB-1995
APPLICATION UNBER: US 08/099,991
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/512,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-782-997A-24
Sequence 24, Application US/08782997A
Patent No. 6030602
GENERAL INFORMATION:
APPLICANT: Legendre, Jean-Yves
APPLICANT: Appended, Andreas
APPLICANT: Tracciak, Andreas
                                                                                                                                                                             US-09-512-983-7; Sequence 7, Application US/U9512983; Patent No. 6265552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
               Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 amino acids
                                                                                                                                                                                                                                                                                                                                        STREET: One Prairie CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-512-983-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Schatz,
                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                      166 QPVAVL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 QPVAVL 171
                                                                                                           2 OPVAVL 7
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 Query Match
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APPLICANT: Gelfand, Erwin W.
TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
TITLE OF INVENTION: GENE RECOMBINATION
TITLE OF INVENTION: Peptide Conjugates for Transfecting TITLE OF INVENTION: Cells NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS: ADDRESSE: HOffmann-La Koche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%; Score 6; DB 3; Length 35; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-100S SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/782,997A FILING DATE: 14-JAN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 28-FEB-1997
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Gaps

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TITLE OF INVENTION: Improved Preparation of Cat Dander TITLE OF INVENTION: Allergens for Immunotherapeutic Purposes and Uses Thereof NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 6; DB 1; Length 70; 100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0; Indels
                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P36,207
ER: IML89-02AA/IPC-002CC/IMI-020
Query Match 2.4%; Score 6; DB 4; Length 38; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/662,193
                                                                                                                                                                                                                                                                                                                                                                                                                           E: LAHIVE & COCKFIELD
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 Sequence 3, Application US/07662193; Patent No. 5328991; GENERAL INFORMATION:
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ative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E. REGISTRATION NUMBER: P36,207 REFERENCE/DOCKET NUMBER: IM TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 3:
                                                                                                                                                                                                                                                                                                APPLICANT: Kuo, Mei-chang
APPLICANT: Bond, Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CRONAN, JOHN E. TITLE OF INVENTION: FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-07-662-193-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 24
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Best Local Similarity ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 LSLLDK 188
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;Patent No. 5252466
                                                                                    12 GVL/TGT 17
                                                                                                                             32 GVLTGT 37
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                                                                                                                                                                                                               US-07-662-193-3
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dreyfus, David H.
APPLICANT: Gelfand, Erwin W.
TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
TITLE OF INVENTION: GENE RECOMBINATION
UMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.4%; Score 6; DB 2; Length 38; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDJUM TYPE: Floppy disk
COMPUTER: JBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sheridan Ross
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2879-39
                                                                                    2879-39
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APPLICATION NUMBER: 08/807,332
FILING DATE: 28-FBB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09338876
Patent No. 6187584
GENERAL INFORMATION:
                                        REGISTRATION NOMBER: 33,005
REGISTRATION NOMBER: 33,005
REFERENCE/DOCKET NUMBER: 287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                               TELEPHONE: 303/869-9700
TELEFAX: 303/863-023
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               LENGTH: 38 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-09-338-876-6
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 GVLTGT 17
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32 GVLTGT 37
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                                                                                                                                                                                                                                                                                                                      US-08-807-332B-6
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CURRENT APPLICATION DATA:

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72 QLAKOK 77
       ;Patent No. 5459046
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US-08-855-531D-9
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                     SEQ ID NO:11
                                                           BACTERIUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A Gene Expression System NUMBER OF SEQUENCES: 185 CORRESPONDENCE ADJRESS: ADDRESSEE: No. 58437020 No. 58437020 No. 5843702th America, Inc. STREET: 405 Lexington Avenue
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                               Ouery Match 2.4%; Score 6; DB 6; Length 75; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3614.214-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: US/08/248,839C
25-MAY-1994
APPLICATION NUMBER: US/07/525,568
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/08248839C Patent No. 5843702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Grodg, Valeta A.
REGISTRATION NUMBER: 35,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                     APPLICATION NUMBER: 354,266
FILING DATE: 19-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       McConnell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Devine, Kevin
O'Kane, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Protein US-08-248-839C-67
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                        166 QPVAVL 171
                                                                                                                                                                                                                                                                                       23 OPVAVL 28
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                                                                                                           LENGTH: 75
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                                                                                          ;SEQ ID NO:3
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5459046-11
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TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL

TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL

RESPONSE AGIANST VIRUSES CAUSING PORCINE RESPIRATORY ANT

REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAIN

A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE

NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
APPLICANT: KODAMA, TOHRU: IGARASHI, YASUO
IITLE OF INVENTION: CYTOCHROME C GENE DERIVED FROM HYDROGEN
                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 80;
0. 2.4e+02;
cches 0; Indels
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REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 4625-038-55X DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,531D
FILING DATE: 13-May-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 6; DB 6
100.0%; Pred. No. 2.4
tlive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/969,071
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTHR: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/U7/943,140
FILING DATE: 10-SEP-1992
PRIOR APPLICATION DATA: 486,409
APPLICATION NUMBER: 28-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08855531D Patent No. 6110467 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PREM, PAUL S.
HALBUR, PATRICK G.
MENG, XIANG-JIN
LUM, MELISSA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 85 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                           NUMBER OF SEQUENCES:
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Matches 6; Conserva
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USA
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                                          US-07-807-529A-4
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APPLICANT: HALBUR, PARTICK G.
APPLICANT: HALBUR, PATRICK G.
APPLICANT: HENG, XIANG-JIN
APPLICANT: HENG, XIANG-JIN
APPLICANT: LUM, MELISSA A.
APPLICANT: LUM, MELISSA A.
APPLICANT: LON, YOUNG S.
TITLE OF INVENTION: VACCINEE RAISING AN IMMUNOLOGICAL
TITLE OF INVENTION: RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND
TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: DELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ASTRET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
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                                                                               Query Match

2.4%; Score 6; DB 3; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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REFERENCE/DOCKET NUMBER: 4625-040-55X DIV
TELECOMMUNICATION INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PULDE ADPLICATION DATA:
APPLICATION NUMBER: US 07/969,071
FILING DATE: 30-0CT-1992
ATTONNEY/AGENT INFORMATION:
NAME: LAVALLEYE, JEAN-PAUL M.P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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LENGTH: 85 amino acids
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
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                       US-08-855-531D-9
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APPLICANT: Garman, Richard D.
APPLICANT: Garman, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Kuo, Mei-chang
APPLICANT: Briner, Thomas J.
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: PEPTIDES USEFUL FOR TOLERIZATION
                                                                                                                                                                                                                                                       TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULGGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
                                                                    APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Greenstein, Julia L.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morvile, Mei-chang
APPLICANT: Morvile, RECOMBITOPE PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: IPC-027/imi-015 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/662,276 FILING DATE: 28-FEB-1991 APPLICATION NUMBER: US 07/431,565
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; Sequence 4, Application US/07807529A; Patent No. 5547669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Channing, Stacey L. REGISTRATION NUMBER: 31,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-807-529A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PER NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                     STREET: Out
                                                    GENERAL INFORMATION:
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APPLICANT: Tan, Faul
APPLICANT: Hiyama, Jun
APPLICANT: Hiyama, Jun
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Schiner, Margot
APPLICANT: Schiner, Margot
APPLICANT: Schinge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 91;
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2.4%; Score 6; DB 2; Les
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                11000.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 143, Application US/08997362 Patent No. 5985287
                                                  NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                            REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1BM Compatible
                                                                                                                                                                                                                                                    91 amino acids
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TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                     linear
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             FILING DATE:
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US-08-997-080-143
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                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
CORRESPONDENCES: 194
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.4%; Score 6; DB 5; Length 88; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DAY:
APPLICATION NUMBER: US/08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                              FILING DATE: 19930325
CLASSIFICATION:
PRIOR APPLICATION LATA:
APPLICATION NUMBER: US 08/006,116
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/884,718
FILING DATE: 15-MAY-1922
APPLICATION NUMBER: 07/857,311
                                                                                                                                                                                                                  SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02462
FILING DATE: 19930325
                                                                                                       ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 143, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/857,311
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mandragouras, Amy E.
RATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARATTERISTICS:
LENGTH: 88 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein
PCT-US93-02462-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2601 E
                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 LSLLDK 81
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                                                                     STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Sequence 143, Application US/09324542
Patent No. 6328978
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/07807529A
; Patent No. 5547669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mycobacterium vaccae US-09-324-542-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rogers, Bruce L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 VTANVT 134
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    45 VTANVT 50
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                                                                                   US-09-324-542-143
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APPLICANT: Visser, Elizabeth
APPLICANT: Visser, Elizabeth
APPLICANT: Prestidge, Ross
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                 2.4%; Score 6; DB 2; Length 91;
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11000.1002c3
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                                                                                                                                                                                                                                                                                                                                       Sequence 143, Application US/09095855 Patent No. 6160093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,007
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/99
FILING DATE: 23-DEC-1997
AUTORNEY/AGENT INFORMATION:
                                                                                              Query Match
Best Local Similarity 100.0
Thus 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-269-0563
                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sleath, Janet REGISTRATION NUMBER:
; TYPE: amino acid
; STRANDEDNESS: sin
; TOPOLOGY: linear
US-08-997-362-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-095-855-143
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                              129 VTANVT 134
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                                                                                                                                                                                                                                                                                                  RESULT 48
US-09-095-855-143
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Gaps
APPLICANT: Watson, James D.
APPLICANT: Tan Paul L.J.
APPLICANT: Tan Paul L.J.
APPLICANT: Tan Paul L.J.
APPLICANT: Tan Paul L.J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Of Immunologically-Mediated Skin bisorders
FILE REFERENCE: 11000.1007-1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 91;
0. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.4%; Score 6; DB 4, Best Local Similarity 100.0%; Pred. No. 2.76 Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Greenstein, John L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morvile, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 07/431,565
03-NOV-1989
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APPLICATION NUMBER: US 07
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
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Channing, Stacey L.

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**REGISTRATION NUMBER: 31,095
**REFERENCE/DOCKET NUMBER: 1PC-027/imi-015
**TELECAMMINICATION: INFORMATION:
**TELEPHONE: (617) 494-0060
**TELEPHONE: (617) 494-0060
**SEQUENCE CHARACTERISTICS:
**SEQUENCE CHARACTERISTICS:
**TYPE: AMINO ACID
**TYPE: AMINO ACID
**TYPE: AMINO ACID
**TYPE: Protein
**SCORE 6; DB 1; Length 92;
**Best Local Similarity 100.0%; Pred. No. 2.8e+02;
**Matches 6; Conservative 0; Mismatches 0; Indels 0;
**Matches 6; Conservative 0; Mismatches 0; Indels 0;
**Search completed: August 6, 2002, 16:46:09
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